Te Niwha
Infectious Diseases
Research Platform

Aotearoa, New Zealand

Infectious Diseases & Pandemic Preparedness Summit 2025

Programme

10 – 13 November 2025,
Tuurangawaewae Marae,
Ngaaruawaahia, Waikato

Kia niwha te ngaakau
ki te whakauu i ngaa mahi
ataawhai moo te iwi.

Be brave and steadfast
to do what is best
for the people.

Kiingi Taawhiao

Welcome

Hutia te rito o te harakeke,
kei hea te Kōmako e kō
Kī mai koe, ki ahau
He aha te mea nui o tēnei ao
Māku e kī atu
He tangata! He tangata! He tangata!

It is a privilege to gather at Tuurangawaewae Marae, where Te Niwha was launched three years ago. This is a place of deep importance within Māoridom and across Aotearoa, and returning here marks a significant milestone for this kaupapa.

As I have stepped into this role, I have had the opportunity to learn about the breadth of work, through Te Niwha, 95 research projects have been funded, involving more than 300 researchers. This mahi has strengthened capability and fostered relationships that are now deeply embedded across the infectious diseases research landscape. I acknowledge and thank all who have contributed their time, effort, expertise, and continued commitment to this shared effort.

This year's Summit 'Celebrating Progress, Building Preparedness' is an opportunity to reflect on what has been achieved so far, and to honour the people who have contributed. It is also a chance to connect, share insights, and reinforce the relationships that support collaboration and preparedness for the future.

I would like to thank Sir Ashley Bloomfield and Dr Martin Gagnon for their steady guidance and support and special thanks to the wonderful Te Niwha team who have made this all happen.

I look forward to the conversations, insights, and connections that will come from our time together at Tuurangawaewae Marae.

Ngā manaakitanga
Maree Roberts
Manu Taupua – Interim Director

Te Niwha
Infectious Diseases Research Platform

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Venue

Tuurangawaewae Marae

Tuurangawaewae Marae was conceived in 1921 by Princess Te Puea Herangi, the granddaughter of King Taawhiao, the second Maaori King. The marae was named Tuurangawaewae, "a place to stand", to emphasise its important strategic role as a place of belonging and a home for many Maaori who were displaced. Princess Te Puea dedicated her life to building Tuurangawaewae Marae and other marae within Waikato's rohe, as well as safeguarding the Kiingitanga and its people. She followed the Pai Maarire faith, opposed conscription in the First World War, and did much to develop an economic base for Waikato Maaori. Following the influenza pandemic of 1918, when a quarter of the population at Mangataawhiri died, Princess Te Puea organised the historic move from Te Paina/Mercer to Ngaaruawaahia. There she established makeshift homes for the many orphans and supporters who followed her, founding Tuurangawaewae Marae. Concerned about future epidemics, she began fundraising for a hospital for Maaori, and this led to the erection of the tuupuna whare at Tuurangawaewae, Maahinaarangi.

Opened in 1929, Maahinaarangi was to provide rongoaa as well as Western medical treatments in a building that looked reassuringly like a meeting house. In the hospital, tikanga would be observed. It would be open to any Maaori, not just those from Waikato. However, it was devastating that, after all of Princess Te Puea's efforts, the application for a licence for Maahinaarangi to be used as a private hospital was declined by the health authorities. Maaori had apparently been refused treatment at Waikato Hospital when it first opened, seeding decades of mistrust in public health services and providing a further argument for a hospital at Tuurangawaewae. After this disappointment, Maahinaarangi was repurposed as a place for Kiingitanga Arikinui to host their manuwhiri. The royal residence, Tuurongo, was later opened in 1938. The marae complex today consists of a number of historic and modern buildings including Ngā Miro Health Centre which was established in 1991. The health centre offers a wide range of services designed to support and empower whaanau to take control of their own health.

Many world leaders, including Nelson Mandela, Queen Elizabeth II, King Charles III and Queen Camilla, have visited Tuurangawaewae Marae. The marae is a site of political diplomacy, and enduring relationships have been established with the royal houses of Tonga, Samoa, Fiji, Hawai'i, Tahiti and the Cook Islands. As a result, during the annual Koroneihana (coronation) festivities, representatives of the Polynesian royal families, including the late Queen Sālote of Tonga and many of her descendants, have made multiple visits and gifted highly prized taonga to Kiingitanga leaders, which are now housed in Maahinaarangi and Tuurongo.

Tuurangawaewae marae is an important gathering place for Maaori throughout Aotearoa; however, it is the responsibility and honour of Waikato Maaori to uphold the mana of Te Arikinui Kuini Ngā Wai hono i te po's principal Kiingitanga marae.

Programme

Monday, 10 November 2025

Pōwhiri

2:45 pm	**Arrive outside Tuurangawaewae Marae**
3:00 pm	**Pōwhiri commences**

Session 1

Grounding the journey

Facilitated by Taki Peeke

4:30 pm	Opening address **Pandemic response - Built on the backs of our ancestors** Professor Marama Muru-Lanning and Dr Te Anga Nathan
5:00 pm	**Mātauranga and Science in action** Maihi Makiha
5:15 pm	**Bridging Knowledge Systems** Facilitated by Dr Raukura Roa
6:00 pm	Session closes

Tuesday, 11 November 2025

MC Dr Raukura Roa

8:45 am	**Karakia**
9:00 am	**Opening remarks** – Sir Ashley Bloomfield

Session 2

Getting ready for the next pandemic

Facilitated by Sir Ashley Bloomfield

How can Aotearoa be ready for the next pandemic? This session explores how science, policy, and communities can work together to prepare for emerging threats like avian influenza. A keynote on pandemic planning with a particular focus on zoonotic threats sets the stage, followed by a panel of experts from across public health, government, research, and clinical care discussing readiness and strengthened preparedness.

9:15 am	**Keynote talk** Professor Nigel French (Distinguished Professor, Massey University and Emeritus Director Tangata Tiriti of Te Niwha)
9:45 am	**Panel Discussion** Dr Emma Sherwood (National Protection Clinical Team, National Public Health Service) Dr Alan Pithie (Chief Medical Officer of Health, Canterbury) Dr Owen Sinclair (Rata Hauora Tamariki/Paediatrician, Te Whatu Ora Waitematā) Paul Bingham (Principal Advisor Animal Health Surveillance, MPI) Dr Sue Huang (Director WHO National Influenza Centre, PHF)
10:30 am	Morning tea

Session 3

Oral presentations

11:00 am	**Stream 1** – Influenza pandemic preparedness Room: Kimikimi, Chair: Professor Nigel French
15 min	**A total system review of infectious disease surveillance in Aotearoa New Zealand** Dr Neilenuo Nelly Rentta
15 min	**Enhancing Respiratory Surveillance: Community Pharmacy-Based Monitoring of Influenza-Like Illness in Aotearoa \New Zealand** Dr Sarah Jefferies, Professor Alex Semprini
15 min	**REMAP-CAP – identifying novel therapeutics for seasonal influenza while preparing for the next global influenza pandemic** Dr Tom Hills
15 min	**Avian influenza virus surveillance across New Zealand and its subantarctic islands** Dr Stephanie Waller
15 min	**Modelling infectious disease dynamics and impact in different ethnicity groups** Professor Michael Plank
Lightning talk	**Strengthening Pandemic Preparedness through Global Collaboration for Vaccine Safety** Melissa Collins

11:00 am	**Stream 2** – Antimicrobial stewardship and therapeutic development Room: Pare Hauraki, Chair: Professor Steve Chambers
15 min	**Reducing antibiotic usage in people with self-limiting viral illness** Dr Mark Thomas
15 min	**Lessons Learned from Establishing Antimicrobial Resistance Genomic Surveillance in Fiji.** Dr Saki Baleivanualala
15 min	**Improving the safety and effectiveness of leprosy treatment in Kiribati through enhanced molecular diagnostics** Dr Patrick Campbell
15 min	**Promoting equitable access to effective treatment for Staphylococcus aureus bacteraemia in Aotearoa; PRobenecid-boosted Oral antibiotic dosing in the SNAP trial (PR-O-SNAP)** Dr Max Bloomfield
15 min	**Repurposing cancer drugs as antivirals** Dr Natalie Netzler
Lightning talk	**Examining host signalling pathway inhibitors for antiviral activities against Zika and dengue viruses** Meghna Patel
Lightning talk	**Exploring the bioactivities of tūpākihi rongoā against viral infection and inflammation** Matija Taaitoa Sucich
Lightning talk	**Identifying novel drug targets in Acinetobacter baumannii using in vitro and in vivo fitness profiling** Janaya Stevenson
12:30 pm	Lunch

Session 4

Turning research into action

Facilitated by Maree Roberts

Policy makers are often under pressure to make timely, evidence-informed decisions that affect public health. This panel brings together policy perspectives on how infectious disease research can be made more accessible, actionable, and aligned with policy needs – offering insights for researchers seeking to turn their rigorous research into real-world impact.

1:30 pm	**Introductory remarks**
1:35 pm	**Speaker perspectives**
	Dr Katherine Gottlieb (former CEO Southcentral Foundation - Nuka System of Care, Alaska) Rangimahora Reddy (CEO, Rauawaawa Kaumātua Charitable Trust)
2:05 pm	**Panel perspectives and discussion**
	Dr Andrew Old (Deputy Director-General, Public Health Agency) Paula Tesoriero (Chief Executive, Whaikaha – Ministry of Disabled People) Dr Willy-John Martin (Director Māori Research, Science, and Innovation, MBIE) Ruth Issac (Deputy Director-General, Strategy and Policy, Ministry of Health) Dr Aumea Herman (Chief Clinical Advisor for Pacific Health, Public Health Agency)

3:00 pm	Afternoon tea

Session 5

Oral presentations

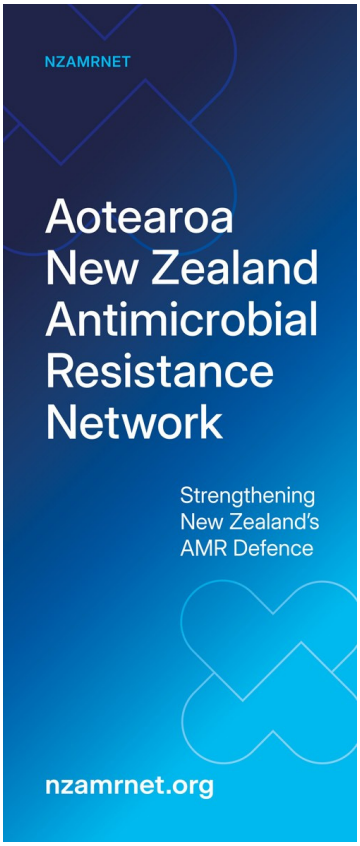
3:30 pm	**Stream 1** – From research with communities to impactful translation Room: Kimikimi, Chair: Dr Joanna Hicks
15 min	**Antibiotic use in Aotearoa** Associate Professor Stephen Ritchie
15 min	**Māori perspectives on antibiotic guidelines use in Aotearoa** Dr Karen Wright, Dr Leanne Te Karu
15 min	**Developing a Kaupapa Māori framework for infectious disease surveillance** Dr Katrina Ford, Dr Tia Dawes
15 min	**SCIP: Convenient and effective treatment for Māori, Pacific Peoples in preventing rheumatic heart disease** Julie Cooper, Associate Professor Julie Bennett
Lightning talk	**Whitia Kia Ora: Indigenous Health Care Model for Rheumatic Fever** Associate Professor Anneka Anderson, Manawa Rhind, Monleigh Ikiua
Lightning talk	**Distributed Real-Time Pathogen Genomic Surveillance at the Point of Need: a Pilot Program at Te Whatu Ora – Capital, Coast & Hutt Valley** Dr Max Bloomfield
Lightning talk	**A scoping synthesis of COVID-19 pandemic preparedness, response, and aspirations among Māori communities.** Dr Ruby Tuesday, Faletoese Asafo
Lightning talk	**Pacific Community Responses to COVID-19 in Aotearoa New Zealand: A scoping synthesis** Dr Ruby Tuesday, Faletoese Asafo

3:30 pm	**Stream 2** – From vaccination research to disease prevention Room: Pare Hauraki, Chair: Professor Alex Semprini
15 min	**Lifting Immunisation in the Tainui Waka Rohe** Shaun Akroyd
15 min	**Modelling the interaction between ethnicity and infectious disease transmission dynamics** Vincent Lomas
15 min	**Epidemiology of Tuberculosis and BCG vaccine uptake among Pasifika in Aotearoa New Zealand** Rhonita Schutz
15 min	**Accuracy of measles serology and post MMR measles antibody responses via alternate vaccine delivery routes** Sumanta Saha
Lightning talk	**Pattern of BCG vaccine-induced protection in peripheral blood** Riya Shajumon
Lightning talk	**Developing a Multisite Database for Background Rates of Adverse Events for Vaccine Evaluation in Africa** Luam Ghebreab
Lightning talk	**mRNA vaccine for protecting immunocompromised tamariki : a qualitative study of parents and caregivers' views** Leia Paltridge

NZAMRNet

Networking event

Tuesday, 11 November 2025, 5:30 PM
WAIKATO TAINUI ENDOWED COLLEGE



Collaborative networking session:
AMR in the Pacific & AMR in the environment

Join us for drinks, nibbles and an interactive Design Solution Lab workshop where researchers, clinicians, and stakeholders unite to tackle the challenges of Antimicrobial Resistance (AMR) in the Pacific and the environment.

This hands-on session, brought to you by NZAMRNet, uses design thinking prompts to spark creativity, foster collaboration, and generate bold, action-able ideas.

About NZAMRNet:
The Aotearoa New Zealand AMR Network (NZAMRNet) is building a multi-stakeholder community dedicated to tackling antimicrobial resistance. Our mission is to foster collaboration, share knowledge, and connect people across disciplines and sectors researchers, clinicians, policymakers, industry, and communities. By creating spaces for dialogue and co-creation, NZAM-RNet aims to break silos and encourage cross-sector partnerships, aligning efforts with regional and global initiatives. Together, we aim to drive research, innovation, and policy solutions that protect health across people, animals, and the environment delivering real impact for Aotearoa and beyond.

What to expect:
Through dynamic, rotating sessions, participants will:

- Identify critical gaps and challenges in AMR across Pacific communities and environmental systems.
- Map capabilities and resources to leverage existing strengths.
- Co-create innovative solutions that can make a real-world impact by 2035.
- Build interdisciplinary teams and explore potential funding pathways to bring ideas to life.

Why attend?

- Expand your network across disciplines and sectors.
- Shape the future of AMR research in the Pacific and environmental contexts.
- Position yourself and your team for future funding and impactful research outcomes.

Complimentary registration required

Wednesday, 12 November 2025

MC Taki Peeke

8:45 am **Karakia**

Session 6

Honouring and celebrating the Te Niwha Journey

Facilitated by Professor Ian Town

This session celebrates the Te Niwha Journey – the Infectious Diseases Research Platform built on partnership, collaboration, and bound by Te Kawenata. The session begins with a keynote reflecting on the platform's development and achievements, followed by stories and insights from Te Niwha–funded researchers. The second half showcases examples of research that bring Te Niwha's vision to life – spanning strategic, Te Ao Māori, and community-led initiatives.

9:00 am **Keynote talk**

Professor David Murdoch (Chief Scientist, PHF Science and Distinguished Professor, University of Otago)

9:30 am **Panel Talks**

A panel of researchers will share a range of insights, learnings and anecdotes from their Te Niwha-funded research.

Nalei Taufa
Mike Edmonds
Erana Kihi
Associate Professor Stephen Ritchie
Dr Natalie Netzler

10:10 am Strategic Project:

Data Sovereignty for Tāngata Whaikaha Māori: Insights from Te Ao Mārama Survey Panel
Associate Professor Andrew Sporle, Taki Peeke

10:25 am Kia Tupu Community Development Project - Lightning talk
Building Resilient Whānau: Lessons from COVID-19 for Future Infectious Disease Preparedness
Ngahiraka Dallas

10:30 am Te Ao Māori Research Priority Theme:
Whiitiki Whakatika
Dr Raukura Roa, Dr Raaniera Te Whata, Hon Nanaia Mahuta, Huirama Matatahi

10:45 am Morning tea

Session 7

Oral presentations

11:15 am	**Stream 1 –** Kia Niwha Fellows' Session Room: Kimikimi, Chaired by the Kia Niwha Fellows
5 min	**Fellowship overview**
15 min	**Grounded in Community: Strengthening Pandemic Preparedness in Indigenous Communities** Dr Fatima Ahmed
15 min	**Indigenous Leadership in Infectious Disease Preparedness: Integrating Sovereignty, Knowledge Systems, and Partnership** Professor Eric Liberda
15 min	**Migration Health Initiative: From Emergency Response to Global Health Equity** Dr William Staufer
Lightning talk	**Inclusive preparedness: Strengthening pandemic plans for migrant and refugee communities** Associate Professor Nadia Charania
Lightning talk	**Antimicrobial resistance and ecosystem health surveillance in freshwater environments** Dr Rose Collis
Lightning talk	**Harnessing the antiviral activities in Pacific traditional medicines** Dr Natalie Netzler
Lightning talk	**Rejuvenating the ageing immune system to improve vaccine efficacy in older people** Dr Theresa Pankhurst
Lightning talk	**Mini-lungs as an airway disease model platform** Dr Andrew Highton
11:15 am	**Stream 2 –** One Health perspectives I Room: Pare Hauraki, Chair: Professor David Murdoch
15 min	**A population-based study of hospitalisation for acute gastroenteric infection in Aotearoa New Zealand (2010-2019)** Dr Alice Hyun Min Kim
15 min	**Drinking water quality and enteric disease: a nationwide case-crossover study (2015–2019) in New Zealand** Associate Professor Tim Chambers
15 min	**Association between heavy rainfall, dairy cattle density and campylobacteriosis (2015-2019)** Professor Simon Hales
15 min	**Spatial Modeling of Campylobacteriosis Notification Rates in Relation to Drinking Water Supply Characteristics** Dr Farnaz Pourzand
15 min	**Emerging Campylobacter species linked to human diseases at a wildlife–livestock–human interface in Uganda** Dr Valter Almeida
12:30 pm	Lunch

Session 8

Oral presentations

1:30 pm	**Stream 1 –** Innovation for better community health Room: Kimikimi, Chair: Professor John Fraser
15 min	**Infectious disease modelling to support communities** Dr Sarah Pirikahu
15 min	**Microbial cell-free DNA: a non-invasive approach to diagnosing infectious diseases** Dr Amy Scott-Thomas
15 min	**Point-of-use testing for infectious diseases in the community** Dr Shirley Keown, Dr Craig Billington
15 min	**Point-of-care testing paired with cervical screening pathways: a study of healthcare delivery in remote Aotearoa** Associate Professor Jo-Ann Stanton
15 min	**Co-development of regional specific frameworks for exploring new anti-microbial and anti-viral agents sourced from taonga herbal remedies** Joanne Murray, Wayne Blissett, Dr Isabel Moller
15 min	**Pacific Cultural Best Practice Approach results to 100% Pacific Participants in Carriage Study** Galumalemana Vaifagaloa Naseri
	Community-Led Approaches to Carriage Surveillance of Infectious Diseases in Te Hiku o Te Ika Conor O'Sullivan

1:30 pm	**Stream 2 –** One Health perspectives II Room: Pare Hauraki, Chair: Dr Rose Collis
15 min	**Vibrio an emerging disease threat for Aotearoa: Hapū focus group findings** Maria Hepi and Mike Edmonds
15 min	**Leptospirosis in Aotearoa: climate-driven outbreaks** Dr Shahista Nisa
15 min	**Para Hopuhopu – Wastewater Epidemiology** Professor Marama Muru-Lanning, Dr Jo Chapman, Dr Brent Gilpin
15 min	**From Global Warming to Local Warning: Climate Health Security and Pandemic Preparedness in Aotearoa/New Zealand** Dr Annette Bolton
Lightning talk	**Roof harvested drinking water surveillance using metagenomics and qPCR in the Ngāi Tahu Takiwā** Gabe Mulcare
Lightning talk	**Linking Treated Water Contamination and Campylobacteriosis Risk Using Explainable Machine Learning** Dr Farnaz Pourzand
3:00 pm	Afternoon tea

Session 9

NGĀTAHI
Research Leaders Forum

Together, as one, in unison.

Facilitated by Professor Steve Chambers

3:30 pm	**Special session** *Meet hip-hop artist Bennett Pomana who will be sharing his experience of sepsis.*
	Unprepared and unaware: knowledge gaps in post-infection, post-sepsis recovery Dr Paul Huggan & Bennett Pomana
followed by	**Poster Session & open Ngātahi Forum – your time and space to meet and mingle** Refreshments available

Poster presentations

P1 **Mass burial and carcass disposal practices during Avian Influenza outbreaks: Enhancing New Zealand's Emergency Preparedness**
Dr Laura Banasiak

P2 **Uncovering virus diversity in urban waterfowl**
Ms Lia Heremia

P3 **Climate variability, seasonal shifts and climate impact on waterborne disease in Aotearoa/New Zealand.**
Dr Annette Bolton

P4 **He Tūāpapa Hauora: Housing-Related Health Outcomes in Te Tai Tokerau – A Mixed Methods Study "A foundation for health"**
Tia Ashby

P5 **Community-Based Carriage of Neisseria meningitidis and Streptococcus pneumoniae in Pacific Households in South Auckland**
Mishal Manisha Naidu

P6 **Molecular characterisation of Streptococcus pneumoniae and Neisseria meningitidis carriage in the community.**
Eszter Scarlett-Herbert

P7 **He aha ngā tikanga hou mo te whakamatautau wai para - New methods for wastewater testing?**
Marama Muru-Lanning, Lynn Lewis-Bevan, Sally Reid

P8 **Registered Nurses' Views on Te Whata Kura: Aotearoa's Antibiotic Guidelines. Exploring Usability, Relevance, Practice Implications**
Dr Gigi Lim, Dr Mark Thomas, Dr Steve Ritchie

P9 **Patient-reported preferences around intravenous and oral antibiotics for the treatment of Staphylococcus aureus bacteremia**
Ms Loughlin McGrath

Poster presentations (continued)

P10 **Antimicrobial Susceptibility of Kingella kingae from Australia and New Zealand: Implications for Paediatric Osteoarticular Treatment**
Ms Katharina Wolf

P11 **Unprepared and unaware: knowledge gaps in post-infection, post-sepsis recovery**
Dr Paul Huggan & Bennett Pomana

P12 **Feasibility of a sustainable community-led response plan for infectious disease**
Ngahiraka Dallas, Dr Irene Setiawan

P13 **Cultural Safety Training for New Zealand Secondary Prophylaxis Providers for Rheumatic Fever**
A/P Anneka Anderson, Mrs Monleigh Ikiua, Mrs Manawa Rhind

P14 **Pacific youth Risk perceptions on Infectious diseases and Social Media – PRISM study**
Jason Tautasi, Luisa Taufa

P15 **16S rRNA sequencing surveillance tool to monitor community drinking water supplies in the Aotea Harbour**
Okeroa Waaka

P16 **Genomic epidemiology of Mycobacterium tuberculosis complex in Fiji**
Dr Saki Baleivanualala

P17 **CRISPR-Cas12a detection of M leprae DNA in human samples for the diagnosis of leprosy**
Dr Amy Scott-Thomas

P18 **Development of a urine-based bacterial cell-free DNA test for Legionnaires' disease**
Dr Amy Scott-Thomas

P19 **Detection of Legionella cell-free DNA in blood for the non-invasive diagnosis of Legionnaires' Disease**
Dr Amy Scott-Thomas

P20 **Mechanisms of immune escape by hypervirulent strains of Mycobacterium tuberculosis**
Dr Naomi Daniels

P21 **Investigating the role of the TNFAIP3 T108A/I207L genetic variant in immune response to infectious disease**
Emma Duffy

P22 **Safety of aH5N6c Influenza Vaccinations in Adults Primed with aH5N1c or Unprimed (V89_18E1)**
Edith Rosenberg

P23 **Immunogenicity of aH5N6c Influenza Vaccinations in Adults Primed with aH5N1c or Unprimed (V89_18E1)**
Edith Rosenberg

P24 **Developing a Multisite Database for Background Rates of Adverse Events for Vaccine Evaluation in Africa**
Dr Luam Ghebreab

P25 **HPV vaccination in Aotearoa New Zealand: Coverage achieved under school-based and primary-care-based programmes.**
Ms Sarah Cosgrove

Te Niwha Summit Dinner

Infectious Diseases Research Platform

Complimentary registration required

5:45 pm	Seated for tea in Kimiora, Tuurangawaewae Marae
6:00 pm	**Summit Dinner** *Join us in celebrating the Te Niwha Journey*

Award of 2025 Scholarships

PhD Scholarship: Okeroa Waaka
PhD Scholarship: Lia Heremia
PhD Scholarship: Gabe Mulcare
Masters Scholarship: Teinatangi Ringi

Thursday, 13 November 2025

MC Dr Raukura Roa

8:45 am	**Karakia**

Session 10

Oral presentations

9:00 am	**Pandemic preparedness –** Thriving together, leaving nobody behind Room: Kimikimi, Chair: Dr Theresa Pankhurst
15 min	**Are we still on target? – insights from ARROW New Zealand** Prof Cameron Grant, Marisa van Arragon
15 min	**Pacific youth Risk perceptions on Infectious diseases and Social Media – PRISM study** Jason Tautasi
15 min	**Empowering Aboriginal (Australia) and Torres Strait Islander Voices Through Involvement and Consultation** Bryony Roberts, Kristy Crooks
Lightning talk	**Māori whānau experiences of critical illness in Wellington Intensive Care Unit** Jackson Smeed-Tauroa
10:00 am	Morning tea

Session 11

Reflections on the future of ID research in Aotearoa

Facilitated by Sir Ashley Bloomfield and Glenda Raumati

10:30 am **Setting the scene**

Facilitated by public health leader Sir Ashley Bloomfield and community health leader Glenda Raumati, this session is dedicated to exploring emerging priorities and future directions for infectious disease research in Aotearoa.

10:45 am **Panel Discussion** – Te Niwha Science Review Team

Through reviewing Te Niwha's Science Excellence over the past months, our panellists gained deep insights into the ongoing research. Hear from these international leaders about opportunities to strengthen research focus, workforce, leadership, and partnerships across sectors in Aotearoa.

Dr Katherine Gottlieb

Professor Paul Kelly

Dr Michelle Linterman

11:15 am **Interactive session**

Discussion stations will provide opportunities to share your perspectives and help shape the future strategy for infectious diseases research in Aotearoa.

12:30 pm **Closing remarks**
Hon. Nanaia Mahuta

12:55 pm **Karakia**

Facilitators and invited speakers Profiles

Panellist - Session 2

Paul Bingham

Paul Bingham is a veterinarian and epidemiologist and has held a number of roles at the Ministry for Primary Industries over the past 20 years. He is currently the Principal Advisor across animal health surveillance and Incursion Investigation in the Diagnostic, Readiness and Surveillance Directorate (DRS). The directorate is, amongst other things, responsible for the timely and accurate detection of exotic and emerging animal diseases, and the design and management of surveys and surveillance programs which allow New Zealand to certify freedom from trade sensitive diseases. Paul has a special interest in disease outbreak investigation.

Facilitator - Sessions 2 and 11

Sir Ashley Bloomfield KNZM

Sir Ashley Bloomfield is Chief Executive at the New Zealand Institute for Public Health and Forensic Science (PHF Science) and Professor at the University of Auckland's School of Population Health. He was appointed a Knights Companion of the New Zealand Order of Merit in 2023 for his services to public health.

With over 25 years' experience in public policy and health leadership - including time at the World Health Organization in Geneva – Sir Ashley Bloomfield is widely recognised for his leadership during New Zealand's COVID-19 pandemic response as Director-General of Health (2018–2022).

Sir Ashley Bloomfield trained in medicine at the University of Auckland and specialised in public health medicine. His professional interests include preventing and controlling non-communicable diseases and addressing health inequities.

Speaker - Session 2

Distinguished Professor Nigel French

Nigel is Distinguished Professor of Infectious Disease Epidemiology and Public Health at Tāwharau Ora | School of Veterinary Science, Massey University and Honorary Professor in the Department of Pathology and Biomedical Science at the University of Otago. He is currently Emeritus Director Tangata Tiriti of Te Niwha, the Infectious Disease Research Platform, and Emeritus Director of the New Zealand Food Safety Science and Research Centre. He was elected as Fellow of the Royal Society of New Zealand in 2014 and made Companion of the New Zealand Order of Merit in 2023 for services to epidemiology.

Facilitators and invited speakers Profiles

Speaker - Session 4, Panellist - Session 11

Dr Katherine Gottlieb

Katherine Gottlieb served Southcentral Foundation [Nuka System of Care], an Alaska Native Regional Healthcare System, as President/Chief Executive Officer for 30 years, departing in 2020. She is a Senior Fellow of Murdock Charitable Trust, Faculty, Harvard Medical School since 2015, awarded 2015 Harry S, Hertz Leadership Award by Malcolm Baldrige National Quality, 2004 MacArthur Genius fellow, honorary doctorates from Alaska Pacific University and the University of Alaska, author of His Hand Upon Me and Psalms of the Heart and Soul and holds a private pilot license. Katherine was inducted into the Alaska Women's Hall of Fame in 2025.

She is a tribal council member of Seldovia Village Tribe, council member of the Seldovia Native Association. Previous Board member of Alaska Native Heritage Center, Alaska Native Tribal Health Consortium, Alaska Federation of Natives, Alaska Pacific University, National Library of Medicine, Cook Inlet Headstart and Storyknife Women's Retreat. Owner of Katherine Gottlieb Strategies, LLC. Current Board member and Chief Executive of Edgenuity.

Panellist - Session 4

Dr Aumea Herman

Dr Herman is a public health physician and general practitioner who holds a PhD in epidemiology from the University of Auckland. Dr Herman was appointed as the Secretary [Director General] of Health for the Cook Islands Ministry of Health in 2018 and helped lead the national emergency health response to COVID-19. In 2023, she received the Pasifika Medical Association Life Member Award for her contribution to Pacific Health. She is the Chief Clinical Advisor for Pacific Health, with the Pacific Health Directorate, Public health Agency, Manatū Hauora Ministry of Health. Since 2024, Dr Herman has been a member of the Te Niwha Steering Committee.

Panellist - Session 2

Professor Sue Huang

Professor Sue Huang, FRSNZ, received her PhD in virology from the University of Pennsylvania, is a globally renowned virologist, particularly influenza and polio viruses. She has been the director of the World Health Organization [WHO]'s National Influenza Centre at the New Zealand Institute of Public Health and Forensic Science [formerly ESR] for over 27 years. She is also the Principal Investigator of the Southern Hemisphere Influenza and Vaccine Effectiveness Research and Surveillance [SHIVERS] program – a long series of research and surveillance on influenza virus, immunity and vaccine.

Facilitators and invited speakers Profiles

Panellist - Session 4

Ruth Isaac

Ruth Isaac brings with her a wealth of experience across the public service. She has held senior roles in government agencies including The Treasury, Ministry of Education, Ministry of Business, Innovation and Employment, and the Department of Conservation.

From 2022 she served as Deputy Director-General for Policy and Regulatory Services at the Department of Conservation, where she led strategic policy, international engagement, Treaty negotiations, legal services, and regulatory functions. This included progressing a major overhaul of the Conservation Act to modernise the system for concessions and generate revenue for maintaining conservation areas.

Ruth is known for her strategic leadership, deep commitment to public policy, and her ability to build high-performing, inclusive teams. Ruth's collaborative working style and strong track record of navigating complex systems will hold her in great stead as she picks up the reins for strategy and policy here at the Ministry of Health.

Panellist - Session 11

Professor Paul Kelly

Professor Paul Kelly is a public health advisor and the former Australian Government Chief Medical Officer and Head of Interim Australian Centre for Disease Control at the Australian Government Department of Health and Aged Care and an Adjunct Professor at the Australian National University. A public health physician and epidemiologist by training, Professor Kelly first joined the Department in March 2019 as the Chief Medical Adviser, Health Products Regulation Group. Professor Kelly was the key medical advisor to the Australian Government during the COVID-19 pandemic and has since advised the Irish Government and the Gulf Centre for Disease Control on health protection and pandemic preparedness.

Professor Kelly has previously worked in research, health systems development, post-graduate teaching and as a health service executive at local, state and national levels in Australia, Malawi, Indonesia, East Timor and the UK.

Professor Kelly has over 35 years research experience and has published over 200 journal articles, book chapters and public health guidelines. He has supervised or mentored many trainees and post-graduate students and delivered lectures, workshops, seminars and conference talks in Australia and internationally.

Facilitators and invited speakers Profiles

Panellist - Session 11

Dr Michelle Linterman

Michelle Linterman is Programme Leader at the Malaghan Institute (Aotearoa New Zealand) and an Associate Group Leader at Babraham Institute (United Kingdom). Her laboratory's re-search focus is on how different cell types collaborate in the germinal centre to generate a ro-bust antibody response following vaccination and infection. Her team's work combines re-search in mice, with human studies to enable delivery of mechanistic insight into the germinal centre response that is of direct relevance to human health.

As an expert on the ageing immune system and vaccination, Dr Linterman is a member of several wider networks, including the Cambridge Immunology Network, GSK Immunology Network, and BBSRC/MRC-CAtalyst Reducing ImmuNe Ageing (CARINA) network, part of the wider UK Ageing Network. She is also a co-leader of part of the UKRI-funded IMMPROVE project to unite global expertise to understand the body's response to COVID-19 vaccines, improve vaccine development and support future pandemic preparedness.

Speaker - Session 11

Hon. Nanaia Mahuta

Ngāti Mahuta | Ngāti Maniapoto | Ngāti Manu

Nanaia Mahuta is a māmā, mentor, strategic adviser, and community researcher with a deep passion for global affairs and indigenous diplomacy.

With 27 years in Parliament, she has been committed to Māori development, foreign affairs, and kaupapa that contribute to being resilient, sustainable and enterprising whānau thriving in their communities. She made history as the first female MP to wear moko kauae in Parliament and later as Aotearoa's first female Minister of Māori Development and Foreign Affairs.

Beyond titles, Nanaia's focus has remained the same—creating pathways for Māori to thrive and amplifying indigenous success on the world stage. From embedding Indigenous values in diplomacy to pioneering Kaupapa Māori Housing, strengthening Pacific partnerships, and advancing Māori and Pasifika representation in governance and procurement, her work has tested the current boundaries and continues to inform her contribution.

At the heart of her journey is a commitment to indigenising decision-making—honoring tūpuna while shaping a mokopuna-centered future for people, the planet, peace, and prosperity.

Facilitators and invited speakers Profiles

Speaker - Session 1

Maihi Makiha

Ko Paguru te maunga
Ko Hokianga te moana
Ko Whakarapa te awa
Ko Waipuna te marae
Ko Ngati Manawa te hapu
Ko Te Rarawa te iwi
Ko Maihi Makiha toku ingoa

Matauranga Māori and western science are vital to the wellbeing of the Taiao. Te Rarawa with the support Ministry for Environment through Te Mana o Te Wai developed a programme “Me He Wai” to support hapū and marae to build their capacity and capability in and make decisions for freshwater management and to improve the health of freshwater bodies of importance to the hapū and marae and create nature - based employment opportunities.

Local knowledge (Nga Kohinga Survey) combined with science (1,2,3 Survey) built a robust knowledge base in the development of the Te Rarawa Taiao Dashboard. All data collected is held under the Data Sovereignty agreement between Te Rarawa and the respective Marae.

The two worlds co excite in Te Taiao let that be an example for the Nation.

Panellist - Session 4

Dr Willy-John Martin

Dr Willy-John Martin (Ngāti Whātua, Ngātiwai, Ngāti Tamaterā, Ngāpuhi) is the Director Māori, Science, Innovation and Technology at MBIE. He has held senior leadership roles across the science system and in Indigenous research. He leads work at the intersection of science policy, research investment, the science system, and mātauranga Māori. On this panel, he brings experience turning evidence into policy, policy into investment, and investment into action.

Speaker - Session 6

Professor David Murdoch

Professor David Murdoch is an infectious disease physician and clinical microbiologist whose career has combined clinical practice, scientific research and senior leadership in both health and academia. He is currently Chief Scientist at the New Zealand Institute for Public Health and Forensic Science (PHF Science) and Distinguished Professor at Ōtākou Whakaihu Waka - the University of Otago.

A former Dean and Vice-Chancellor of the University of Otago, Professor Murdoch is internationally recognised for his contributions to pneumonia research, the development of diagnostic tools for infectious diseases, and vaccine policy.

Facilitators and invited speakers Profiles

Speaker - Session 1

Professor Marama Muru-Lanning

Professor Marama Muru-Lanning is a social anthropologist at the University of Auckland. She also Chairs the Waikato-Tainui Endowed College for Research and Development. Her scholarship is dedicated to transdisciplinary research with Māori communities that prioritises tikanga, equity, inclusion and interdependence. Over the past ten years she has also developed a passion and advanced new approaches and methods for conducting research with kaumātua.

Marama is from Turangawaewae Marae, a marae that is a potent living memorial to the many Waikato Māori who succumbed to the Spanish Flu pandemic of 1918. She has whakapapa that connects her to Waikato, Ngāti Maniapoto and Ngāti Whātua

Speaker - Session 1

Dr Te Anga Nathan

Dr Te Anga Nathan is a transmedia storyteller and researcher of Te Aupōuri, Ngāti Porou, and Waikato descent. With more than three decades of experience in journalism, broadcasting, and public relations, he has contributed extensively to advancing Māori media. He recently earned his PhD at Te Whare Wānanga o Awanuiārangi, where his research developed the Māui Mataora model to guide the live streaming of tangihanga with integrity.

Panellist - Session 4

Dr Andrew Old

Dr Andrew Old is a public health physician with over 20 years' experience in clinical leadership, executive management, and governance across strategy, community participation, patient experience, and quality improvement. A 2018/19 Commonwealth Fund Harkness Fellow, he was based at Standford University and UC San Francisco before returning to support New Zealand's COVID-19 response as Chief Clinical Officer for the Northern Region. He later became the inaugural Deputy Director-General of the Public Health Agency in 2022. A graduate of the University of Auckland and Fellow of the Australasian Faculty of Public Health Medicine, Andrew was awarded Fellowship of the New Zealand Medical Association in 2011 for his services to the profession and the public.

Facilitators and invited speakers Profiles

MC - Monday and Wednesday

Taki Peeke

'Ko taku mana ko te ataarangi o ōku kawaitanga hei kahukōrako ki te hunga hauā' - The reflections of my ancestry grounds and guides what I do.

Taki's introduction to disability began in 1985 as a kaitiaki through a head injury disabling his grandfather and his ability to live independently including tribal and cultural responsibilities. In 1989 Taki volunteered at the local day base of IHC where he has recently finished as their national Māori advisor. Taki has been a board member of Te Ao Mārama Aotearoa Trust since 2018.

Panellist - Session 2

Dr Alan Pithie

Dr Alan Pithie is the chief medical officer for Canterbury/Waitaha. He brings a wealth of international and local experience to the role, having started his medical career as a house officer in Glasgow, Scotland, in the early 1980s. He trained in general medicine and infectious diseases/tropical medicine and held numerous leadership roles over the last 26 years in Canterbury. He was also the clinical lead who managed the Canterbury response to the Covid pandemic between 2020 and 2023 and was the deputy CMO from 2023 until March this year.

Facilitator - Session 11

Glenda Raumati

Waikato, Ngati Mutunga

Glenda Raumati is General Manager of Ngaa Miro Health in Ngaaruawaahia. A member of Waikato Tainui Whanau Ora collective, the Whānau Ora provider is based at Tuurangawaewae marae where Glenda is also a Trustee.

Glenda has worked in the service of her community and its health for over 25 years and is a strong proponent of the vision set by Te Puea Herangi to care for our people across all aspects of their life.

Facilitators and invited speakers Profiles

Speaker - Session 4

Rangimahora Reddy

Originally from Himatangi, Rangimahora has worked for Rauawaawa Kaumātua Charitable Trust since 2010. Working with Kaumātua or those she describes as "nga matauranga taonga" makes Rauawaawa a very special place to be. Rangimahora has been educated at Massey University and has spent the last three decades working in both the health and education sectors.

Speaker - Session 1, MC - Tuesday and Thursday

Dr Te Raukura Roa

Iwi: Ngāti Maniapoto, Ngāti Hauā, Ngāti Korokī-Kahukura.
Mahi: Director of Roa Limited, Teaching and Research Contractor

Te Raukura o Te Rangimarie Roa is a teacher, a researcher, and an author of children's te reo Māori books. She has been a Fulbright Scholar in Residence at the University of Hawai'i at Mānoa, an Erskine Scholar at the University of Otago, and a Te Wheke a Toi Post-Doctoral Fellow at the University of Waikato. She is currently contracted as a researcher on the Whiitiki Whakatika research project, is researching the impacts of Māori language trauma in language acquisition, and is teaching te reo Māori at government organisations, iwi, hapū, and Marae wānanga reo.

Ko te pae tawhiti, kia manawa-roa ai te reo Māori i roto i ngā horopaki katoa o te ao. Ko te pae tata, kia kimi rongoa e manawa-ora ai te reo Māori i roto i ngā horopaki katoa o Aotearoa.

Facilitator - Session 4

Maree Roberts

Maree is Te Niwha's Manu Taupua - Interim Director. She brings extensive experience in public policy, having held several senior roles across government over the past 15 years. Most recently, she served for six years as Deputy Director-General of Strategy, Policy and Legislation at the Ministry of Health, where she played a key role in both the COVID-19 response and the recent health reforms.

As a policy professional, Maree is deeply committed to ensuring that research translates into meaningful, positive change for New Zealanders. Maree will also provide strategic leadership to steer the next phase of infectious disease research in Aotearoa New Zealand, ensuring a strong connection between evidence and impactful action.

Facilitators and invited speakers Profiles

Panellist - Session 2

Dr Emma Sherwood

Emma Sherwood is a Medical Officer of Health in the National Protection Clinical Team, National Public Health Service (Health New Zealand | Te Whatu Ora), where she is clinical lead for avian influenza and pandemic preparedness. As a UK trained doctor, Emma held roles in the UK including Clinical Lead for the COVID-19 Therapeutics Programme at the UK Health Security Agency and Registrar to the Chief Medical Officer at the Department of Health and Social Care. Emma moved to Aotearoa New Zealand with her whānau in 2022, where she has a held a variety of roles including within the National Public Health Service.

Panellist - Session 2

Dr Owen Sinclair

Ko Owen Sinclair Taku ingoa
Ko Te Parawa te Iwi
He Rata Hauora Tamariki ahau

I am a paediatrician working at waitakere hospital one of only 13 Maori paediatricians in Aotearoa. I am the current president of Te kahui matai o arotamariki o Aotearoa / The paediatric society of New Zealand. I am the current co-chair of the national immunisation taskforce and the norther regional immunisation governance group. I lecture in ethnic inequalities in health at Waipapa Taumata Rau. i am currently conducting research into the ongoing effects of Measles and respiratory disease in tamariki. I have been a vocal advocate in mutiple forums and media for addressing ethnic discrepancies of health outcomes in Aotearoa.

Facilitators and invited speakers Profiles

Panellist - Session 4

Paula Tesoriero MNZM PLY

Paula is well-known and a respected leader in the disability community. She is disabled and has a deep knowledge of the challenges and opportunities for the disability community.

Paula is a Paralympian, winning a gold medal and two bronze medals at the 2008 Summer Paralympic Games in Beijing.

Paula is currently the Chief Executive of Whaikaha-Ministry of Disabled People, the first Ministry of its kind in the world working to achieve better outcomes for disabled people in New Zealand.

Paula was previously the Disability Rights Commissioner at the Human Rights Commission, a position she held since 2017. She also acted in the role of Chief Human Rights Commissioner from May 2018 – January 2019.

Paula has served in various governance roles including as Deputy Chair of Peke Waihanga — Artificial Limb Service and Deputy Chair of Nuku Ora (previously Sport Wellington) and she served on the Board of Paralympics NZ. She is a life trustee of the Halberg Disability Sport Foundation and is an honorary advisor to the Asia New Zealand Foundation.

Facilitator - Session 6

Professor Ian Town

Ian Town is the Chief Science Advisor at the Ministry of Health. Ian Town has worked across both the health and education sectors during his 30-year career. A physician by training, he has published extensively in respiratory medicine. Much of this research has been implemented through evidence-based guidelines for the management of common conditions such as asthma, COPD and pneumonia. Following an 8-year period at the University of Canterbury as Deputy Vice-Chancellor he had a wide range of roles including Chair of the PBRF Sector Reference Group and Chair of the TEC PBRF Governance Group overseeing the 2018 Quality Evaluation. He completed a 5-year term as the Chair of the Health Precinct Advisory Council leading one of the key Christchurch recovery projects. In his role at Chief Science Advisor, he is part of the Strategy and Policy Group working to ensure that science and evidence are at the core of the Ministry's work.

Abstracts

Session 3 – Stream 1

A total system review of infectious disease surveillance in Aotearoa New Zealand

Neilenuo Nelly Rentta[1], Celia Hume[1], Sarah Pirikahu[1], Amanda Kvalsvig[1], Michael Baker[1]
1 University of Otago, Wellington, New Zealand

Background: Infectious disease (ID) surveillance plays a crucial role in protecting public health, including detecting disease outbreaks and potential pandemics as well as monitoring ID epidemiology and the impact of interventions. Aims: 1) To systematically describe all of the ID surveillance syste in Aotearoa New Zealand (NZ) in 2025 according to 13 major functional ID categories and points in the causal path (disease, hazards/protections, interventions, determinants), 2) To compare the current scope of ID surveillance with a review done in 2010 to identify how surveillance has changed over this 15-year period and 3) To identify strengths and gaps in the current scope of ID surveillance where improvements are needed.

Methods and preliminary results: We conducted a review of literature and reports from key agencies responsible for ID surveillance in NZ. Key findings were systematically recorded in tabular form that listed all discrete surveillance systems. We identified IDs of interest and whether these are currently covered by existing ID surveillance syste and strengths and gaps identified by topic experts and key end users. We used our novel surveillance sector review framework for reviewing and assessing the performance of these syste and whether they are meeting end user needs. Our preliminary findings show close to 150 ID surveillance syste are currently functioning in NZ. Over the last 15 years the overall number of ID surveillance syste has increased by more than 30% with increases seen across most categories.

Discussion and initial recommendations: In NZ, ID surveillance is carried out mostly by a range of government agencies. Academic/other groups run around 10% of ID surveillance systems. Some of these syste operate in silos with duplication in some areas and no clear central leadership. We will present recommendations for achieving a more cohesive approach to ID surveillance that better meets the need of end users.

Enhancing Respiratory Surveillance: Community Pharmacy-Based Monitoring of Influenza-Like Illness in Aotearoa New Zealand

Sarah Jefferies, Alex Semprini, Kyley Kerse, Gabrielle Shortt, Melemafi Porter, Andrea McNeill, Richard Beasley, Allie Eathorne, Ben Waite, Lauren Jelley, Selwyn Te Paa, Trisha Falleni, Kerry Dean, Marylin Loe, Nicholas Shortt, Alex Martin, Bianca Black, Shirena Vasan, Martin Lowis
1 Medical Research Institute of New Zealand, Wellington Regional Hospital, New Zealand

Community virological influenza-like illness (ILI) surveillance across Aotearoa New Zealand is currently undertaken through the PHF Science led, Sentinel General Practice Respiratory Virus Surveillance (SGPRVS) network. Many NZ patients face barriers to accessing healthcare, such as geographic isolation, limited GP capacity and cost, therefore existing surveillance may not represent the true circulating viral burden in the community, impacting public health response. Community pharmacies present an opportunity to enhance the detection of circulating viruses via expansion of the sentinel virological surveillance network.

This feasibility study is assessing community pharmacy participation in national ILI virological surveillance through the Pharmacy Research Network (PRN). 477 adults presenting to community pharmacies with WHO-defined ILI sympto (fever ≥38°C, cough and onset >10 days) are being recruited across two winter seasons (weeks 18-39 of 2024/2025) and the inter-seasonal period. Pharmacists collect nasopharyngeal swabs for testing by PHF Science using RT-PCR. The primary outcome is the proportion of positive samples. Secondary outcomes include the proportion positive for the different viruses assessed, comparison with SGPRVS data, demographic representation, and acceptability scores from participants and pharmacy investigators.

To August 2025, 354 participants have been swabbed, with study completion expected before 29th September 2025. Of the PRN-collected swabs analysed, 52% tested positive for a respiratory virus of interest with the following distribution (inclusive of co-infections): influenza A and rhinovirus (33% each), followed by influenza B (7.7%), SARS-CoV-2 (7.7%), human metapneumovirus (6.5%), RSV (6.5%), parainfluenza virus type 1-3 (4.8%), adenovirus (2.4%) and enterovirus (0.6%). 71.5% of participants are European, 19.4% Māori, 12.5% Asian, 5.1% Other/MELAA and 3.4% Pacific Peoples. No adverse events have been reported. Data collection will be complete for the Summit and presented alongside the concurrent SGPRVS data.

This feasibility study represents the first systematic assessment of community pharmacy-based respiratory surveillance using gold standard nasopharyngeal swabbing techniques and RT-PCR.

REMAP-CAP – identifying novel therapeutics for seasonal influenza while preparing for the next global influenza pandemic

Tom Hills[1,2], Anthony Jordan[3], Colin McArthur[3]
1 Medical Research Institute Of New Zealand, Wellington, New Zealand, 2 Te Whatu Ora – Health New Zealand Counties Manukau, Auckland, New Zealand, 3 Te Whatu Ora – Health New Zealand Te Toka Tumai, Auckland, New Zealand

REMAP-CAP continues to evaluate a range of treatments for patients hospitalised with respiratory infections. Our Te Niwha mahi addresses three key clinical questions within this adaptive platform trial:

1. Do corticosteroids, effective in severe COVID-19, improve outcomes in severe influenza?
2. Do immunomodulatory agents, effective in severe COVID-19, improve outcomes in severe influenza?
3. Does antiviral therapy, including combination antiviral therapy, improve outcomes in severe influenza?

Recruitment update: Globally, REMAP-CAP has recruited 15,512 participants, with Aotearoa New Zealand achieving the highest per capita recruitment. In 2025 to date, the Aotearoa New Zealand REMAP-CAP Team have enrolled 90 patients with severe pneumonia and influenza in intensive care units (ICUs) and expanded to enrol 39 patients hospitalised with severe influenza outside ICU.

Representativeness and outcomes: Health equity, including in trial participation is a core focus. In collaboration with the University of Auckland Department of Statistics, we compared REMAP-CAP randomised trial participants with registry patients admitted to the same ICUs meeting the same inclusion and exclusion criteria but not enrolled. Age and sex distributions were closely matched (mean age 62 vs 63 years; 65% vs 66% male). Māori and Pacific Peoples were well-represented: 26.7% and 10.8% of trial participants identified as Māori and Pacific Peoples, respectively, versus 23.5% and 13.2% of registry patients. In-hospital mortality was 1.3% (7/559) for REMAP-CAP participants and 3.8% (19/512) for registry patients. The unadjusted risk ratio for mortality in REMAP-CAP participants compared with registry patients was 0.35 (95% CI 0.15–0.80), suggesting substantially lower odds of death in the randomised group. However, only 28 in-hospital deaths were observed and measures of severity of illness were not available for this preliminary analysis. We plan to extend this to include a broader range of clinical, physiological, and laboratory variables, and to examine mortality beyond the index hospital stay.

Avian influenza virus surveillance across New Zealand and its subantarctic islands

Stephanie Waller[1], Jemma Geoghegan[1]
1 University of Otago, New Zealand

Highly pathogenic avian influenza (HPAI) H5N1 virus has never been detected in New Zealand. Its introduction would be catastrophic for the country's poultry, livestock, and native avian and marine mammal species. Migratory birds are a key route through which HPAI H5N1 could enter New Zealand. Despite this risk, little is known about the viruses that naturally circulate in New Zealand's wild birds and how these viruses are transmitted between these species. Surveillance efforts have largely focused on mainland waterfowl neglecting New Zealand's offshore and subantarctic islands which host a diverse range of avian species. To expand our knowledge of avian influenza viruses across New Zealand, we sampled wild aquatic birds from New Zealand, its outer islands and subantarctic territories. Metatranscriptomic analysis of 700 individuals spanning 33 species revealed no detection of HPAI during the annual 2023-2024 migration. However, a single detection of low pathogenic avian influenza (LPAI) H1N9 was found in red knots (Calidris canutus) at the Firth of Thames, a key site at the terminus of the East Asian-Australasian Flyway that hosts thousands of migratory birds annually. In addition, we uncover the global connectedness and transmission pathways of other avian viruses harboured in these species, highlighting the potential risk for a HPAI incursion. This research provides a foundation for improved avian influenza monitoring and deepens our understanding of the evolutionary dynamics of avian influenza viruses across New Zealand.

Modelling infectious disease dynamics and impact in different ethnicity groups

Michael Plank[1], Samik Datta[2], Andrew Sporle[3]
1 University of Canterbury, Christchurch, New Zealand, 2 Earth Sciences New Zealand, Wellington, New Zealand, 3 iNZight Analytics, Auckland, New Zealand

Most compartment-based infectious disease models tend to ignore social variables such as ethnicity and socioeconomic position. However, these can be key determinants of disease transmission and impact in heterogeneous populations. Accounting for these effects is crucial in models that are designed to be used for policy advice and decision support. This project ai to develop infectious disease models that stratify the population by ethnicity, and to use these models to explore drivers of inequities in disease impact. Using the Omicron period of the Covid-19 pandemic in Aotearoa New Zealand as a case study, we

investigate the relative contributions of disparities in vaccination rates, clinical risk and contact patterns to observed epidemiological trends. Definitively disentangling these factors is difficult with available data, but we conclude that while vaccination rates contributed to inequitable outcomes, these are not sufficient to fully explain observed data on Covid-19 outcomes. It is likely that higher contact rates for Māori and Pacific populations meant these groups were heavily impacted in the first Omicron wave. While differences in contact rates may have diminished over time, differences in clinical risk continue to contribute to inequitable disease burden in the longer-term. This work is an important step towards models that are better equipped to support a more equitable public health response to future pandemics and emerging infectious disease threats.

Strengthening Pandemic Preparedness through Global Collaboration for Vaccine Safety

Melissa Collins[1]
1 Global Vaccine Data Network, Global Coordinating Centre, Auckland UniServices Limited at University of Auckland, Auckland, New Zealand

Background: The Global Vaccine Data Network (GVDN) is a multinational collaboration advancing vaccine safety and effectiveness science. Rapid vaccine deployment and the emergence of rare Adverse Events of Special Interest (AESIs) during COVID-19 challenged policymaker capacity and public confidence, highlighting the need for timely, high-quality vaccine safety data. GVDN unites global partners and fosters locally led capacity building to address this need, developing contextually relevant evidence to guide effective pandemic responses and strengthen public trust.

Methods: GVDN is a coordinated network of 35 international institutions utilising standardised methods, comprehensive linked health datasets, active surveillance studies and culturally sensitive engagement strategies. Administrative support, data aggregation and meta-analyses is led by GVDN's Global Coordinating Centre (GCC) based at the University of Auckland, with publicly accessible data dashboard creation an essential aspect of the approach.

Results: GVDN's approach has enabled robust evaluation of vaccine safety signals from populations totaling over 300-million individuals. Key findings, including the detection and contextualisation of rare AESIs such as myocarditis and Guillain Barre Syndrome, can inform health policy and risk communication.

Significance: GVDN's model demonstrates that inclusive, globally harmonised vaccine safety monitoring is both feasible and essential for future pandemic resilience and assessment of rare vaccine events. Aotearoa's contribution, through the GCC and local partnerships, is critical in advancing this international effort and shaping regional safety surveillance, providing unique opportunities for local researchers/agencies to co-design and leverage global vaccine safety studies.

Future Directions: GVDN ai to build capacity in LMICs and establish collaboration with Pacific partners - enhancing equitable access to surveillance tools, harmonising health data through a common data model to accelerate aggregated analysis and dissemination of results, as well as developing culturally competent communication/outreach methods. Additionally, AI-driven analysis of social media and other data sources will enable earlier detection of emerging vaccine safety concerns, supporting timely and locally relevant public health responses.

Session 3 – Stream 2

Reducing antibiotic usage in people with self-limiting viral illness

Thomas MG, Arroll BA, Best E, Chan AHY, Fraser L, Reid S, Thaggard S, Wells S, White C, Whittaker R, Wu Z, Ritchie SR

Aims: To determine the impact of a suite of evidence-based interventions on rates of antibiotic prescribing for patients with upper respiratory tract infections presenting to primary care.

Methods: The selection, design and delivery of an evidence-based intervention to encourage reduced antibiotic prescribing for patients with URTIs was discussed with six GPs during three online workshops.
The intervention consisted of a suite of tools that practices and GPs could use at their discretion. These included: providing patients with online access to a broad range of educational resources (in six languages) on best care for people with URTIs; a paper form on which patients could indicate their expectations of their GP consultation; waiting room posters that affirmed prescribers' intentions to only prescribe antibiotics when they were indicated; provision of 29 infographics and 8 videos about the best care for patients with URTIs; a template for prescription of evidence based, non-antibiotic treatments for patients with URTIs; and monthly feedback to each GP on their rate of antibiotic prescribing for patients with URTIs. Antibiotic prescribing rates of participating GPs for patients presenting for a URTI were recorded in 2024 immediately after deployment of the intervention and compared with rates from 2023 and 2019.

Results: 77 GPs in 16 practices provided consent to participate and were included in the study. There were a total of 15,898 GP consultations between July and December for patients presenting with an URTI: 4,752 in 2019; 5,829 in 2023; and 5,317 in 2024. The overall rates of antibiotic prescribing for patients presenting with a URTI, during baseline period 1 (2019), baseline period 2 (2023), and the intervention period (2024) were: 47.9%, 46.3% and 43.5% respectively. There was an approximately 6.5% relative reduction in the rate of antibiotic prescribing between 2023 and 2024 (p=0.02).

Conclusions: Provision of a suite of evidence-based resources was d with an overall approximate 3% absolute and 6.5% relative reduction in the rates of antibiotic prescribing to patients with URTI. This effect was achieved with minimal disruption and essentially no cost for the participating GPs. The study interventions could be readily provided to a high proportion of GPs across NZ at minor cost.

Lessons Learned from Establishing Antimicrobial Resistance Genomic Surveillance in Fiji

Saki Baleivanualala[1,2], Adriu Sepeti[2], Swastika Devi[2], Sajnel Sharma[3], Jesse Martin[4], James Ussher[1,4]
1 Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand, 2 Fiji National University, Suva, Fiji, 3 Ministry of Health and Medical Services, Suva, Fiji, 4 Awanui Labs, Dunedin Hospital, Dunedin, New Zealand

As the hub of the Pacific, Fiji plays a critical role in regional health security and is increasingly recognised as a hotspot of antimicrobial resistance (AMR). This has led to the establishment and operationalisation of a national A genomic surveillance system as part of the Te Niwha funded A reference laboratory and pathogen genomics capability project.

Using Oxford Nanopore Technology (ONT), the system targets WHO critical priority pathogens, including carbapenem resistant Acinetobacter baumannii, Pseudomonas aeruginosa and Enterobacterales. Samples from all major public and private hospitals are centralised under standardised protocols, ensuring consistency in processing and comparability of data nationwide. Genomic sequencing is complemented by phenotypic antimicrobial susceptibility testing, including evaluation of novel antimicrobials, creating an integrated platform for outbreak detection, transmission mapping and evidence based public health action.

Lessons learned during implementation are presented here to support other countries in similar contexts to adapt and replicate this model. Key lessons include the value of proactive engagement with external stakeholders, including ministries of health, hospital leadership, international collaborators and regional public health networks, to secure alignment, resources and long-term commitment. Adapting laboratory infrastructure to meet ONT requirements in a small island setting was essential, ensuring reliable environmental controls and power supply. Building capacity through hands on training, ongoing mentorship and involvement of healthcare essionals in interpreting genomic results has fostered strong local ownership. Addressing logistical barriers from overseas supplier reliance, extended shipping times and custo clearance required forward planning and local stockpiling. Establishing secure data management syste has strengthened trust, reporting efficiency and collaboration. Long term sustainability will depend on stable funding, integration of genomics into routine surveillance and strengthened regional partnerships.

Fiji's model provides a practical and adaptable blueprint for Pacific Island Countries and other resource limited settings facing A threats.

Improving the safety and effectiveness of leprosy treatment in Kiribati through enhanced molecular diagnostics

Patrick Campbell[1,2], Taulanga Naniseni[3], Allison Miller[1], Erei Rimon[3], Nabura Ioteba[4], Trevor Anderson[5], Arturo Cunanan[6,7], Temea Bauro[3], Martin Kennedy[1], Nick Douglas[2,8,9], Stephen Chambers[1]
1 Department of Pathology and Biomedical Science, University Of Otago, Christchurch, New Zealand, 2 Department of Infectious Diseases, Christchurch Public Hospital, Christchurch, New Zealand, 3 Government of the Republic of Kiribati Ministry of Health and Medical Services, Tarawa, Kiribati, 4 Pacific Leprosy Foundation, Christchurch, New Zealand, 5 Canterbury Health Laboratories, Christchurch, New Zealand, 6 Department of Health, Culion Sanatorium and General Hospital, Culion, Philippines, 7 Division of Programmes for Disease Control, Manila, Philippines, 8 Department of Medicine, University of Otago, Christchurch, NZ, 9 Division of Global and Tropical Health, Menzies School of Health Research, Charles Darwin University, Darwin, Australia

Background: Kiribati has one of the highest rates of leprosy in the world. Leprosy treatment requires prolonged multidrug therapy, potentially complicated by leprosy reactions and medication-related adverse events. Specifically, glucose-6-phosphate dehydrogenase (G6PD) deficiency and HLA-B*13:01 allele carriage can predispose to dapsone-induced haemolytic anaemia and dapsone hypersensitivity syndrome (DHS) respectively, contributing to poor compliance and treatment defaults. Antimicrobial resistance (AMR) in M. leprae is rising globally. A monitoring and screening for risk factors for treatment related adverse

events may improve the safety and efficacy of leprosy control programmes.

Methods: Baseline A in M. leprae was determined using nested/heminested PCR assays targeting resistance determining regions for rifampicin (rpoB), dapsone (folP1) and fluroquinolones (gyrA) of M. leprae DNA in skin biopsies from patients between 2018-2024. Duplicate testing using Deeplex Myc-Lep® next generation sequencing assay is being undertaken to compare the sensitivity of both methods, identify additional resistance markers and for strain identification. Population prevalence surveys for G6PD deficiency and HLA-B*13:01 alleles were conducted using fingerprick blood samples with G6PD activity assessed using the SD biosensor® point of care test, and HLA-B*13:01 testing using a TaqMan based real-time PCR on dried blood spots.

Results: Dapsone resistance was identified in 10/140 (7%) M. leprae isolates. Amongst 339 participants screened, there was no severe G6PD deficiency (<30% activity) whereas intermediate G6PD deficiency was detected in 2/112 (1.8%) females screened. To date, 253 blood spots have been tested with one definite and two possible carriers of the HLA-B*13:01 allele detected.

Conclusions: A moderate level of dapsone resistance in M. leprae is present in Kiribati, highlighting the need for ongoing surveillance. Detection of resistant strains has facilitated individualised treatment and enhanced supervision of affected patients. The burden of leprosy reactions in Kiribati is significant but dapsone-induced haemolysis and DHS are unlikely to be major contributors to these reactions.

Promoting equitable access to effective treatment for Staphylococcus aureus bacteraemia in Aotearoa; PRobenecid-boosted Oral antibiotic dosing in the SNAP trial (PR-O-SNAP)

Max Bloomfield

Staphylococcus aureus bacteraemia (SAB) is a common and lethal disease in Aotearoa, which disproportionately affects the very old, the very young, Māori, and Pacific Peoples. Currently accepted treatment involves prolonged intravenous (IV) antibiotic treatment, often for several weeks. In regions with less access to home IV therapy services, particularly smaller and more rural centres, this may confine patients to prolonged hospitalisation, away from whānau and other supports. Probenecid is a repurposed drug, which, when given in combination with oral beta-lactam antibiotics, reduces kidney excretion of the antibiotic, thereby increasing blood levels. Preclinical evidence suggests that blood levels approaching those achieved by IV treatment can be achieved with oral probenecid beta-lactam combination therapy (PCT). If this can be demonstrated in a robust clinical study it would permit many patients to be treated at home with oral antibiotic therapy, instead of requiring IV.

PR-O-SNAP is an embedded sub-study within the global SAB trial known as SNAP. Patients enrolled in SNAP that meet eligibility criteria will be approached for participation in PR-O-SNAP, whereby they will have blood samples collected during the IV and oral antibiotic treatment phases of their SAB treatment. This will permit comparison of drug levels achieved in patients on IV beta-lactam, oral beta-lactam alone, and PCT. The oral beta-lactam agents begin studied are flucloxacillin, cefalexin, and amoxicillin, which represent the three commonest agents in use. These agents are also in common use for conditions other than SAB, meaning the results of PROSNAP will be applicable to many serious bacterial infection syndromes commonly seen in Aotearoa and abroad.
Recruitment began in June 2024. Middlemore, Wellington, Hutt Valley and Tauranga Hospitals have contributed participants to the study. At time of abstract submission 107 participants had been enrolled, including 40 patients in the cefalexin PCT group, which represents complete enrolment to this group. We are planning our first major analysis of stored blood samples in August and hope to be able to present the results of this analysis at the Summit.

Repurposing cancer drugs as antivirals

Natalie Netzler[1], Qian (Claire) Wang[1,2], Jinchao Xing[3], Chuen-Fuk Chan[4], Nanjun Chen[5], Ashley Nutsford[1,2], Blake Sullivan-Hill[1,2], John Taylor[1,6], Gordon Rewcastle[7], Jack Flanagan[2,7,8], Peter Shepherd[1,2]
1 Faculty of Medical Health Sciences, Waipapa Taumata Rau | University Of Auckland, Grafton, Auckland, New Zealand, 2 Maurice Wilkins Centre, Auckland, New Zealand, 3 Institute of Infectious Diseases, Shenzhen Bay Laboratory, Shenzhen,, Guangdong 518000, China, 4 Jiangsu Provincial University Key (Construction) Laboratory for Smart Diagnosis and Treatment of Lung Cancer, Duke Kunshan University, Kunshan, China, 5 City University of Hong Kong Shenzhen Research Institute, Shenzhen, China, 6 School of Biological Sciences, University of Auckland, Auckland, New Zealand, 7 Auckland Cancer Society Research Centre (ACSRC), Auckland, New Zealand, 8 Department of Pharmacology & Clinical Pharmacology, School of Medical and Health Sciences, University of Auckland, Auckland, New Zealand

Viruses and cancer both disrupt and hijack cellular pathways in our body to support viral replication and to evade the immune response. One central pathway that controls growth, survival, metabolism and the immune response is called the phosphatidylinositol-3-kinase (PI3K) signalling pathway. This pathway has been shown to be hyperactivated by cancer, and therefore drugs

that block or inhibit this pathway have been shown to be effective chemotherapy treatments.
Similar to cancer, many viruses that cause disease are known to switch on this PI3K pathway, to help them multiply and spread. As with cancer treatments, some PI3K inhibitors have been shown to work as antivirals, stopping viruses from causing infection and multiplying.

We examined a panel of PI3K inhibitors in various stages of clinical development at the Auckland Cancer Society Research Centre, to identify those that have broad-spectrum antiviral activities. We selected a suite of PI3K inhibitors to investigate for antiviral effects against diverse viruses including herpes simplex virus Type 1 (causes cold sores), four variants of SARS-CoV-2 (causes COVID-19), common cold coronavirus OC43 and RSV, using gold-standard virology techniques and immunohistochemistry to examine mechanis of antiviral activity.

One lead compound (C20) showed broad-spectrum antiviral activities across all viruses examined with potency in the low micromolar range (1.03 μM -10.10 μM). While C20 had a narrow selective window, it was synergistic in combination with clinically approved antivirals remdesivir, acyclovir and nirmatrelvir (Bliss scores: 13.1-18.0), allowing for dose reductions. This lead has also been shown to be tolerable in clinical trials and animal models.

This study demonstrates the therapeutic potential of repurposing PI3K inhibitors for treating viral infections, which could offer a broad-spectrum antiviral solution for newly emerging viral threats as well as current viral diseases.

Examining host signalling pathway inhibitors for antiviral activities against Zika and dengue viruses

Meghna Patel[1], Ashley Nutsford[1,2], Blake Sullivan-Hill[1,2], Peter Shepherd[1,2], Natalie Netzler[1,2]
1 Department of Molecular Medicine and Pathology, Faculty of Medical and Health Sciences, Waipapa Taumata Rau, Auckland, New Zealand, 2 Maurice Wilkins Centre of Research Excellence, Auckland, New Zealand

Dengue and Zika viruses cause significant health threats, with over 14 million dengue cases and over 44,000 Zika cases reported globally in 2024. These cases are expected to rise worldwide, including Aotearoa. However, we currently lack safe and effective antivirals to combat the severe health burden created by these viruses.

This project ai to identify novel antivirals that target host signalling pathways in our cells that these viruses commonly hijack to replicate and spread. Two of the several pathways investigated in this project are phosphatidylinositol 3-kinase (PI3K), and Ataxia-telangiectasia mutated and Rad3-related (ATR). Strong evidence suggests that temporarily blocking these specific host pathways with inhibitors can reduce viral replication and help the immune system clear the virus.

A panel of host PI3K and ATR pathway inhibitors will be tested against dengue or Zika viruses through plaque reduction assays to find compounds that reduce viral infection. These lead compounds will be analysed further to understand their selective window (safe dose range) and how they work. Assays like immunohistochemistry, time of addition, and Terminal deoxynucleotidyl transferase dUTP Nick-End Labelling (TUNEL) will be used to examine their mechanism of action.

The preliminary assays from this project show that at least one lead compound is worth additional examination as a potential antiviral. Continued investigation will determine which lead compounds are worth developing further into safe and effective antivirals. Such antivirals are urgently required to fight the current and growing threat of Zika and dengue viruses globally. Thus, this project will explore the potential of host pathway inhibitors as antivirals against dengue and Zika viruses.

Exploring the bioactivities of tūpākihi rongoā against viral infection and inflammation

Matija-Taaitoa Sucich[1,2], Kimiora Henare[1,3], Eileena Sucich[2], Jewel Sucich[2], Peter Shepherd[1,3], Natalie Netzler[1,3]
1 Department of Molecular Medicine & Pathology, FMHS, Waipapa Taumata Rau, Taamaki Makaurau Auckland, Aotearoa New Zealand, 2 Ngāti Kuri, Tai Tokerau, Aotearoa New Zealand, 3 Maurice Wilkins Centre of Research Excellence, Aotearoa New Zealand

Tūpākihi (Coriaria arborea) is a rongoā Māori with powerful medicinal effects used for centuries to treat inflammation, pain, strains, and bone fractures. Despite these medicinal uses, Europeans reported it as poisonous to humans and cattle, suggesting the plant›s eradication. For this reason, expert guidance is necessary to navigate the poisonous and medicinal properties. While other closely related Coriaria species have been studied, there has been limited focus on tūpākihi, which may offer the potential solutions for combatting viral skin infections and cellular inflammation.

This study ai to use co-designed methods and tikanga to collect and extract medicinal parts of tūpākihi and expand our mātauranga Māori of tūpākihi rongoā.

Tūpākihi was collected and prepared in Te Hapua by members of the Sucich whānau (Aperahama, Romana, Paraone). The rongoā was sterilised for use in our biomedical assays. The anti-viral activities of tūpākihi extracts were examined against herpes simplex virus type 1 (HSV-1) using viral plaque reduction assays. Cytotoxicity of the extracts was also examined using cell viability assays. Investigations into the anti-cancer properties and anti-inflammatory effects will broaden our understanding of tūpākihi rongoā. Further investigations into any biological impacts of the extracts will be examined using Western blots or apoptosis assay techniques.
While there was no significant antiviral effect detected in plaque assays against HSV-1 in vitro, we are currently examining the tūpākihi extracts for their anti-inflammatory activities in cell-based models. This work is ongoing, and as cell viability was not significantly impacted in cytotoxicity assays, this holds promise for further anti-inflammatory testing of extracts.

Tūpākihi holds significant cultural and spiritual importance for many Māori, linking whenua and ancestral practices. This study of tūpākihi will deepen our understanding and connection to the whenua, allowing us to cast our net into Te Ao o Rongoā to broaden our perspectives of this rongoā rākau.

Identifying novel drug targets in Acinetobacter baumannii using in vitro and in vivo fitness iling

Janaya Stevenson[1]
1 University of Otago, Dunedin, New Zealand

Skin and soft tissue infections are an emerging concern in Aotearoa, disproportionately affecting Māori, particularly tamariki in urban areas. Acinetobacter baumannii, a leading cause, is highly drug-resistant and difficult to treat. Infections are often severe, especially in immunocompromised individuals or those with chronic wounds. Rising resistance highlights the urgent need for novel therapeutic targets. This study ai to identify essential genes that contribute to the survival and persistence of a highly virulent A. baumannii strain (Ab5075). We employed transposon sequencing (Tn-seq), using a T26 transposon mutant pool to assess gene essentiality in two clinically relevant conditions: an in vitro biofilm model and an in vivo murine skin abscess model. Transposon insertion sites were mapped using high-throughput Illumina sequencing to identify genes required for bacterial fitness under each condition. Identifying conditionally essential genes may help reveal promising targets for therapeutic development. The long-term goal is to contribute to novel antimicrobial discovery and help address existing health inequities by targeting pathogens that disproportionately affect Māori populations.

Session 5 – Stream 1

Antibiotic use in Aotearoa

Stephen Ritchie[1], **Emma Best**[1], **Max Bloomfield**[3], **Stephen Chambers**[2], **Tim Cutfield**[3], **Eamon Duffy**[3], **Lily Fraser**[4], **Sharon Gardiner**[3], **Thomas Hills**[3], **Gigi Lim**[1], **Sarah Metcalf**[3], **Alesha Smith**[2], **Leanne Te Karu**[1], **Mark Thomas**[1], **Karen Wright**[1]
1 University Of Auckland, 2 University of Otago, 3 Te Whatu Ora, 4 Turuki Healthcare

The incidence of infectious disease in Aotearoa/New Zealand is grossly inequitable; however, little is known about the equity of antibiotic use. This is an important consideration as antibiotic resistance has the greatest adverse effect on populations who require antibiotics the most. Antibiotics are amongst the most commonly used medicines, but their use is not always appropriate – existing data shows that both under-prescribing and over-prescribing are common. Current data about Aotearoa's antibiotic use is piecemeal and not available in a form that concisely documents what antibiotics are used, by whom and for what conditions. This information is essential for future efforts to improve the equity and appropriateness of antibiotic use. Appropriate use of antibiotics is defined as use that is concurrent with Te Whata Kura, a new national antibiotic guideline developed as part of this project. We have sought to develop data strea to better understand antibiotic use as a proof-of-concept. Prescribing data was obtained from the Medicines Data Repository and from hospital e-prescribing systems, which were also used to derive the reasons for antibiotic use in hospital inpatients. In primary care we have extracted data from practice management syste from practices affiliated with our three partner primary health organisations. The indication for antibiotic use in primary care will be determined using natural language processing of clinical notes. This presentation will discuss the use of antibiotics in primary and secondary care. We will also discuss the future directions for this project.

To date, efforts to support appropriate antibiotic use in Aotearoa/New Zealand have been hampered by a lack of infrastructure: up-to-date data about antibiotic use, and a nationally accepted antibiotic guideline. Our project has filled these two crucial gaps and the infrastructure we have developed can be built upon to enable future research to ensure appropriate antibiotic use.

Māori perspectives on antibiotic guidelines use in Aotearoa

Karen Wright[1], Lily Fraser[2,3], Leanne Te Karu[1], Jennifer Woods[1], Gigi Lim[1]
1 University of Auckland, Auckland, New Zealand, 2 Turuki Health Care, Auckland, New Zealand, 3 Te Hā o Maru, Oamaru, New Zealand

Māori in Aotearoa experience large and persistent infectious disease health inequities. Hospitalisation rates for Māori are more than twice those of non-Māori, non-Pacific peoples. While it is clear that risk and protective factors for infectious diseases are differentially distributed by ethnicity, access to timely, appropriate health care and appropriate antibiotic prescribing also contributes to health inequities. Antibiotic guidelines are used by prescribers to support appropriate antibiotic prescribing and best practice treatment decisions, yet there is little research exploring community and whānau Māori perspectives on their use in clinical interactions.

We are seeking to strengthen antibiotic stewardship and support equitable, appropriate antibiotic prescribing in Aotearoa through a Te Niwha-funded research project. The project includes the development of national antibiotic guidelines (Te Whata Kura) for use across all ages and prescribing settings. This presentation will describe preliminary findings from a qualitative research project aiming to explore Māori perceptions of antibiotic guideline use in primary care. Kaupapa Māori provides a framework for research that is grounded in te Ao Māori, seeking to produce research that is transformative and of benefit to Māori. Findings from focus groups with Māori who engage with primary health care will be shared, providing insights into previous experiences, use in treatment consultations, and areas for future research. This study fills a research gap and will inform understanding regarding antibiotic guideline use, whānau satisfaction, and equitable, appropriate prescribing.

Developing a Kaupapa Māori framework for infectious disease surveillance

Katrina Ford[1], Tia Dawes[1], Hector Kaiwai[1], Noella Taiapa[1], Temi Allison[1], Sarah Pirikahu[2]
1 Wai Rangahau, Te Whānau o Waipareira, 2 University of Otago

The study seeks to understand the needs of Māori communities in protecting themselves against infectious disease (ID), and to develop a kaupapa Māori ID surveillance framework that centres whānau priorities in responding to ID outbreaks and future pandemics. We held wānanga with whānau from communities across Te Ika-a-Māui to ascertain their priorities and concerns. We also interviewed kaimahi from kaupapa Māori health and social service providers and public health essionals in various roles throughout the ID surveillance system to gather their insights and information needs. Findings reveal that many whānau Māori are disconnected from the information pathways and health institutions on which the current ID surveillance system depends. This means whānau are not receiving timely and appropriate information about ID, nor is their experience of ID being captured and reflected in the surveillance data. Kaimahi and public health essionals also face significant barriers in accessing relevant and timely data, particularly immunisation information, which hinders their ability to protect whānau. The current ID surveillance system is failing to meet the needs of many Māori communities. Some of this failure is due to a lack of effective data circulation, where critical information fails to reach those who need it most. However, a more fundamental issue is the current ID surveillance system's individualised focus, which overlooks collective, whānau-centred perspectives. The surveillance system also fails to incorporate mātauranga Māori and the holistic understandings of health and disease that firmly shape Māori conceptions of wellbeing. A kaupapa Māori framework for ID surveillance, grounded in the principles of manaakitanga, whanaungatanga and kaitiakitanga, has the potential to transform how ID is monitored in Aotearoa, for the benefit of all communities.

SCIP: Convenient and effective treatment for Māori, Pacific Peoples in preventing rheumatic heart disease

Julie Cooper[1], Julie Bennett[1], Monleigh Muliaumasealii[2], Dhevindri Moodley[1], Jacqui Ulugia[3], Anneka Anderson[4]
1 Department of Public Health, University of Otago, Newtown, Wellington, New Zealand, 2 National Hauora Coalition, 3 Te Whatu Ora, 4 Faculty of Medical and Health Sciences, Te Kupenga Hauora Māori, University of Auckland

Background: Acute Rheumatic Fever (ARF) and Rheumatic Heart Disease (RHD) remain significant health issues for Māori and Pacific communities in Aotearoa New Zealand. Subcutaneous injection of penicillin (SCIP) enables injections every 10 weeks, an alternative to the standard four-weekly intramuscular (IM) injections. As part of a Phase II SCIP trial, this study explores treatment adherence, pain management, and quality of life for Māori and Pacific participants and their whānau (family), focusing on culturally responsive care. The study builds on prior research that demonstrated clinical viability.

Methods: A Kaupapa Māori and Pacific-centered approach was used, with semi-structured interviews conducted with 10 whānau, including nine participants on SCIP. Data collection occurred between March and August 2024. Thematic analysis was performed to identify key themes from participants' experiences.

Results: Six themes emerged: Reduced burden of treatment, emotional impact from reduced injection frequency, whānau-centered care, Whakawhanaungatanga (relationship building), health literacy, and pain management. Participants reported significant improvements in quality of life, valued SCIP's flexibility, allowing injections at home, work, or school, with the added convenience of visits every 10 weeks. Strong relationships with healthcare providers, especially research nurses, were essential for adherence. Emotional burdens, such as stress d with frequent injections were reduced with SCIP.

Conclusion: SCIP was well received by participants, offering reduced pain, greater flexibility, and an improved quality of life. Whānau involvement and culturally responsive care were central to positive experiences and supported better adherence. Building on these findings, there is an opportunity to expand both locally and nationally, ensuring equitable access for communities most affected by rheumatic fever. Future research should explore how SCIP can be adapted for use in diverse global healthcare settings.

Whitia Kia Ora: Indigenous Health Care Model for Rheumatic Fever

Anneka Anderson[2], **Manawa Rhind**[1], **Monleigh Ikiua**[1]
1 National Hauora Coalition, Auckland, New Zealand, 2 University of Auckland, Auckland, New Zealand

Acute rheumatic fever (ARF) is an inflammatory autoimmune reaction that occurs as a result of a Group A Streptococcus (GAS) infection. Acute rheumatic fever (ARF) remains a critical issue in Aotearoa New Zealand (AoNZ), particularly among Māori and Pacific children aged 5 to 14 years who experience disproportionately high rates. To prevent further heart damage, ARF patients receive monthly intramuscular penicillin injections for a minimum of 10 years. However recent research highlights a gap between ARF services and patients/whānau expectations, creating barriers to accessing and engaging with services. This disconnect contributes to recurrences of ARF and increased incidence and severity of its sequalae rheumatic heart disease (RHD). This research ai to bridge these gaps by developing, implementing and evaluating a Māori and Pacific rangatahi (youth) centered model of care in the Waikato region of AoNZ, using a mixed methods kaupapa Māori approach. This presentation will highlight the key themes Identified by rangatahi and whānau to improve current bicillin delivery, including the importance of agency, whanaungatanga (rapport) and how even the little things, like chocolate fish, can make a big difference for rangatahi.

Distributed Real-Time Pathogen Genomic Surveillance at the Point of Need: a Pilot Program at Te Whatu Ora – Capital, Coast & Hutt Valley

Max Bloomfield

Transmission of pathogenic micro-organis is known to occur in the hospital environment. This can result in outbreaks that cause harm to patients and huge disruption to healthcare services. Outbreak investigations have typically been 'reactive' in nature, triggered when a problem has become large enough to be detected by standard surveillance mechanisms. Confirmation of an outbreak has typically involved sending organis to the reference laboratory for typing, with a turnaround time often measured in weeks. This severely limits the ability of hospital Infection Prevention and Control (IPC) tea to deploy agile, informed responses.

Next Generation Sequencing (NGS) provides high-resolution typing of possible outbreak organisms. It has typically been performed in research or reference laboratory environments due to high costs and complexity. This landscape is rapidly changing, and NGS is now becoming more accessible to front-line clinical diagnostic laboratories. In 2022, Awanui Labs Wellington and Te Whatu Ora – Capital, Coast & Hutt Valley established NGS on site at Wellington Regional Hospital, with collaborative support from ESR/PHF Science. This NGS program had two main functions: 1) to perform real-time genomic surveillance of key hospital pathogens, permitting a 'proactive' approach to outbreak detection and management; and 2) to provide access to rapid 'reactive' NGS when possible outbreaks had been detected via other channels.

In this talk I will share some of our experiences with this program, where NGS results can now be provided to IPC tea within hours, as opposed to weeks, and several outbreaks have been detected and effectively managed at very early stages. I will also discuss our recent adoption of a 'distributed' approach to bioinformatic analysis, which permits rapid cloud-based data sharing between laboratories. This approach has significant potential to provide rapid responses to the significant dual infectious disease threats of antimicrobial resistance and future pandemics.

A scoping synthesis of COVID-19 pandemic preparedness, response, and aspirations among Māori communities

Amio Matenga-Ikihele[2], Faletoese Asafo[1], Joscelin Taugasolo[2], Rihi Marama-Fisher[1], Ruby Tuesday[1]
1 Moana Connect, Māngere, Auckland, New Zealand, 2 Faculty of Medical and Health Sciences, University of Auckland, Auckland, New Zealand

Māori communities across Aotearoa New Zealand demonstrated rapid, culturally grounded responses to the COVID-19 pandemic, often outperforming mainstream syste in agility and community reach. This paper synthesises evidence from iwi response plans and research literature to identify key themes, enablers, barriers, initiatives, and recommendations that shaped Māori-led responses. Key enablers included strong iwi leadership, culturally responsive approaches, community networks/ partnerships, and whānau centred support systems. Māori-led initiatives - ranging from marae-based health services to iwi checkpoints - highlighted the effectiveness of Indigenous-led public health strategies. While positive results were achieved, barriers such as structural and systematic inequities, health access and service gaps, digital exclusion and information barriers, socio-economic hardship, cultural disruption and wellbeing impacts, and funding and resource allocation challenges were noted. Aspirations for future preparedness include embedding tikanga Māori into national emergency planning, improving digital infrastructure, ensuring flexible funding for Māori providers, and strengthening co-governance. These findings affirm the need for structural change to ensure Māori leadership is central to future pandemic preparedness.

Pacific Community Responses to COVID-19 in Aotearoa New Zealand: A scoping synthesis

Amio Matenga-Ikihele[2], Faletoese Asafo[1], Ruby Tuesday[1]
1 Moana Connect, Māngere, Auckland, New Zealand, 2 Faculty of Medical and Health Sciences, University of Auckland, Auckland, New Zealand

COVID-19 exposed deep inequities in health syste globally and in Aotearoa New Zealand, with Pacific communities experiencing a disproportionate burden of illness, economic hardship, and social disruption. Despite these challenges, they filled major gaps in health services, communication, and economic support, and demonstrated resilience, culturally grounded leadership, and the ability to meet community needs through collective action. This qualitative review of 26 peer-reviewed literature, government reports, and community-led research identified five interconnected themes: (1) community partnerships; (2) Pacific centred approaches; (3) clear and trusted communication; (4) digital inclusion and literacy skills; and (5) economic support and sustainability.

Enablers, included community leadership, trusted communication strategies, and agile local systems, alongside barriers such as underinvestment, digital exclusion, reliance on unpaid labour, and limited inclusion of Pacific leadership in early planning. The findings highlight that Pacific-led syste are not supplementary but essential public health infrastructure. Embedding these approaches within national emergency planning, through sustainable funding, formal governance roles, strengthened digital inclusion offers a pathway to a more equitable, trusted, and resilient pandemic response.

For future emergency responses, Pacific-centred approach must be integrated into national planning from the start. This includes sustainable funding, formal leadership roles, and decision-making that reflects Pacific values such as care, reciprocity, and collective responsibility. Planning should happen in clear stages, with everyone involved early on. It's also important to include children and young people, not just as helpers, but as leaders. Their voices and ideas can help build trust, improve communication, and make communities more prepared for future pandemics.

Session 5 – Stream 2

Lifting Immunisation in the Tainui Waka Rohe

Shaun Akroyd[1]
1 Te Rau Ora, Hamilton, New Zealand

Aim: Understanding how and to what extent health service delivery to mokopuna and whaanau across the Tainui waka rohe can be optimised and lift immunisation rates for tamariki 0-5 years old.

Brief methods: Te Niwha have partnered with Te Rau Ora to deliver Raakai, an immunisation evaluation project throughout the Tainui waka rohe. Taking a tikanga-led approach and leveraging the tools of evaluation, we are working with Kaupapa Maaori providers and whaanau to bring forward insight to optimise health service delivery to mokopuna and their whaanau, and test ways that may improve access to immunisation and d health and information services. We are also gathering whaanau data to

understand whaanau attitudes, behaviours and decision-making around immunisation.

Clear results: We have captured Whaanau insights through a range of methods (e.g. whaanau survey, whaanau and provider interviews, podcasts, literature review). Shared insights include:

- Whaanau attitudes, behaviours and decision-making around immunisation
- Insights about the immunisation ecosystems, barriers, enablers and opportunities to reaching whaanau around immunisation

Conclusions or significance of findings:

- Taking a kaupapa Maaori tikanga-led approach to engaging iwi/providers/communities creates trusted relationships, and honours providers by being cognisant of the contexts in which providers operate, which values providers but can take longer to engage
- Factors like respect for whaanau decision-making, improving whaanau access to information and trusted sources of information and preferred service preferences can influence whaanau informed decision-making
- Those who may be vaccine hesitant trust wider whaanau, kaumaatua and friends as trusted people who can provide immunisation information, while still supporting and encouraging other whaanau to make their own decisions
- Whaanau who choose not to vaccinate appreciate having their choices respected and this can seem not to be the case when providers have health targets to meet around vaccination

Modelling the interaction between ethnicity and infectious disease transmission dynamics

Vincent Lomas[1,2], Tim Chambers[2], Michael Plank[1]
1 School of Mathematics and Statistics, University of Canterbury, Christchurch, New Zealand, 2 Ngāi Tahu Research Centre, Christchurch, New Zealand

During the COVID-19 pandemic, Aotearoa followed an elimination strategy followed by a mitigation strategy, which saw high success and kept health impact low. However, there were inequities in health outcomes, notably that Māori and Pacific Peoples had lower vaccine coverage and experienced higher age-standardised rates of hospitalisation and death. Models provide predictions of disease spread and the burden of disease, which can effectively inform policy, but are often not good at including inequities/heterogeneity. Despite the differences in health outcomes by ethnicity, most models have not explicitly considered ethnic heterogeneities as factors and as such were unable to answer import questions during the pandemic. We a model that explicitly considers ethnic effects to investigate the first Omicron wave of the COVID-19 pandemic in Aotearoa, which was the first time there was widespread community transmission of SARS-CoV-2. We then analysed three methods of analysing contact patterns within and between ethnic groups: proportionate mixing, assortative mixing, and empirically derived mixing; and fit them using ethnicity-specific data on reported cases and spatially disaggregated population counts. We found that Māori, Pacific, and Asian contact rates were between 1.17-2.46, 1.60-3.89, and 0.83-0.92 times the European rates, respectively. We then found that from the parameters considered in the model, the disparity in transmission rates explained the majority of the observed disparity in attack rates, while assortativity and vaccine rates explained comparably less.

Epidemiology of Tuberculosis and BCG vaccine uptake among Pasifika in Aotearoa New Zealand

Rhonita Teresa Schütz[1], Taniela Lolohea[1], Janine Paynter[2], Nadia Charania[1]
1 Auckland University of Technology, New Zealand, 2 University of Auckland, New Zealand

The Pasifika population in Aotearoa exhibit unique vulnerabilities that increase susceptibility to TB. This study aimed to identify improvements for TB prevention efforts for Pasifika. Te Kora framework guided a convergent parallel mixed methods study. To understand the epidemiology of TB and the BCG vaccine uptake, a quantitative observational study was undertaken. Concurrently, a qualitative interpretive descriptive study involving maroro (conversations) with healthcare essionals was conducted.

The quantitative results showed that Pasifika and Asian populations had the highest TB incidence rates from 2006 to 2023, with average incidence rates of 11.4 per 100,000 (CI: 8.2 – 15.3) and 27.5 per 100,000 (CI: 23.5 – 32) respectively. TB incidence was higher among smaller Pasifika ethnicities such as Kiribati, Tokelau, Tuvalu and Niue. The average BCG vaccination rate for Pasifika was 519.4 (CI: 500.3 – 539.3) per 100,000, however, based on the significant decrease from 2011 to 2023 which reached vaccination rates as low as 26.6 per 100,000 (CI: 21.7 – 32.2), the Pasifika population were significantly under-vaccinated. Pasifika ethnicities were proportionately vaccinated relative to their population sizes except for the Cook-Island Māori and Niuean ethnicities. Thus, an increase of BCG vaccine uptake for Pasifika, particularly the less dominant Pasifika ethnicities, is crucial.

Three categories from the qualitative data outlined barriers for the BCG programme and TB prevention efforts. Firstly, systemic gaps in identifying at-risk groups such as knowledge gaps among healthcare workers and fragmented referral processes. Secondly, perceptions of TB and BCG vaccine among migrants and Pasifika communities, identified stigma and migrants' percep-

tion of TB risk. Lastly, there were system-based factors such as the BCG programme changes, the Pasifika umbrella and effective communication. These findings support system-level improvements for TB prevention among Pasifika, such as enhancing risk assessment training, uniform referral processes, disaggregated data and health promotion to target TB stigma.

Accuracy of measles serology and post M measles antibody responses via alternate vaccine delivery routes

Sumanta Saha[1], Melanie Millier[1], James Ussher[1], Hinke ten Hulscher-van Overbeek[2], Rob van Binnendijk, Peter McIntyre
1 University of Otago, New Zealand, 2 National Institute for Public Health and the Environment, The Netherlands

Background: New Zealand is the only country which serologically tests all young adults enrolling in tertiary health-related courses irrespective of previous doses of measles, mumps, and rubella (MMR) vaccine. In our study of M delivered by intramuscular (IM), intradermal (ID), and aerosol (AE) routes, we used a bead-based multiplex immunoassay (MIA) to compare Me antibody responses and to investigate an antibody threshold for Me protection.

Methods: Eligible students were ≥18 years and had received two previous M doses. In 2021, we compared % of students Me and/or mumps (Mu) - and Me+/Mu - by the routine test with the "gold standard" PRNT, closely correlated with MIA. In 2023, we used randomised students requiring M (Me and/or Mu -) to IM, ID or AE and gave M by AE to Me and Mu + students. Outcomes were % with ≥4-fold post/pre-M Me Ab rise and post/pre Me geometric mean titre (GMT) ratios.

Results: In 2021, 35/45 (78%) of test – were + by PRNT and 4/39 (9%) of test + were PRNT -. In 2023, Me Ab by MIA pre and post M compared in 190 students (median age:19 years) IM =118 (62.1%), ID 25 (13.3%), AE 47 (24.7%). Pre-M GMTs (IU/ml) were similar. Post M ≥4-fold Ab rise: IM = 39 (33.1%, 95% CI: 25.1, 42.1), ID = 4 (16.0%, 95% CI: 5.8, 37.0), AE: 15 (31.9%; 95% CI: 20.0; 46.8). Post/pre GMT ratios in the lowest pre-M tertile: IM: 4.9 (95% CI: 3.4, 6.9), ID: 4.0 (95% CI: 1.9, 8.1), and AE: 17.1 (95% CI: 8.2, 35.6).

Conclusion: In young adults with vaccine-acquired Me immunity, accuracy of routine serology was poor. Using MIA, Me Ab responses were not significantly different overall but in the lowest pre-M Me Ab, Ab responses were significantly higher with AE delivery.

Rethinking Needle Length: Assessing the Role of Injection Route in COVID-19 Vaccine Response

Melemafi Porter[1,2], Gabby Shortt[1,2], Nicholas Shortt[1,2], Kyley Kerse[1,5], Leanne Liu[4], Thomas Hills[1,5,9], Bianca Black[1], Erasmus Smit[6,7], Lesley Gray[5], Allie Eathorne[1], Richard Steele[8], Sarah Burge[8], Mark Weatherall[1,5], Richard Beasley[1,2,3]
1 Medical Research Institute Of New Zealand, Lower Hutt, Wellington, New Zealand, 2 Victoria University of New Zealand, Wellington, New Zealand, 3 Wellington Hospital, Capital, Coast and Hutt Valley DHB, Wellington, New Zealand, 4 Alexander Pharmacy, Wellington, New Zealand, 5 University of Otago, Wellington, New Zealand, 6 Institute of Environmental Science and Research, Porirua, New Zealand, 7 Virology and Immunology Department, LabPLUS, Auckland City Hospital, Auckland, New Zealand, 8 Immunology Department, Awanui Laboratories, Wellington, New Zealand, 9 Auckland City Hospital, Te Whatu Ora Te Toka Tumai, Auckland, New Zealand

Intramuscular (IM) injection into the deltoid muscle is the recommended route for COVID-19 vaccines. However, previous MRINZ research shows that standard 25mm needles may be insufficient to achieve IM delivery in up to 45% of adults with obesity. Despite national guidelines recommending longer 38mm needles for "very large or obese" individuals, unclear criteria and reliance on vaccinator discretion mean that less than 2% of COVID-19 vaccinations in Aotearoa New Zealand have used longer needles, far below the 34% adult obesity prevalence. Therefore, there is a substantial population in Aotearoa inadvertently receiving their COVID-19 vaccines into the subcutaneous tissue. This issue is exacerbated for Māori and Pacific peoples who face higher obesity rates and vaccine-preventable disease burden. In some vaccines, SC administration is d with reduced immunogenicity and increased local reactogenicity. Whether this applies to COVID-19 vaccines remains unknown.

This randomised controlled trial investigates the impact of injection route on COVID-19 vaccine immunogenicity and reactogenicity. Four hundred adults with obesity were recruited via 14 community pharmacies across Aotearoa through the Pharmacy Research Network. Participants were randomised 1:1 to receive a COVID-19 booster via a 12.7mm or 38mm needle for SC and IM delivery respectively. The primary outcome is SARS-CoV-2 neutralising antibody titres at 28 days post-vaccination. Secondary outcomes include local and systemic reactions are assessed via electronic diaries.

Recruitment is complete and participant follow-up is ongoing. This is the first trial internationally to compare SC and IM COVID-19 vaccination in a real-world, pharmacy-based setting. Findings will directly inform immunisation policy and needle length guidance, with implications for improving vaccine effectiveness, safety, and equity across Aotearoa and internationally.
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Clinical Trial Registration: ANZCTR: ACTRN12624000294550

Pattern of BCG vaccine-induced protection in peripheral blood

Riya Shajumon[1], **Mae Gilmour**[1], **XinYue Wang**[1], **James Ussher**[1], **Naomi Daniels**[1], **Gergely Toldi**[2], **Joanna Kirman**[1]
1 Dept of Microbiology and Immunology, **Ōtākou** Whakaihu Waka, University of Otago, Dunedin, Otago, New Zealand, 2 Liggins Institute, Waipapa Taumata Rau, University of Auckland, Auckland, Auckland, New Zealand

Tuberculosis (TB) caused by Mycobacterium tuberculosis (Mtb) is the leading single-cause infectious killer worldwide. The Bacillus Calmette-Guérin (BCG) vaccine is ~80% effective in children but only has ~50% efficacy against TB in adults, who account for ~90% of TB cases. A novel, more effective, vaccine is desperately needed. A major hurdle facing the development of a new vaccine, is the lack of BCG-related immune correlates of protection, making the testing of novel vaccines difficult.

Lineage 2 – Beijing (L2-B) strains of Tuberculosis are evasive to the protection induced by the BCG vaccine. Identifying how these strains circumvent BCG-induced immunity, could improve our understanding of how the BCG vaccine provides protection against Mtb. For this purpose, mice were vaccinated either intranasally or intravenously with BCG and challenged with either L2-B or Lineage 4 (L4) Mtb. RNA-seq of blood samples taken before and after infectious challenge in vaccinated mice, revealed significant differences in gene expression between the L2-B and L4 challenge.

A comprehensive flow cytometry panel has been developed for use on clinical samples, informed by findings from the mouse study, targeting key immune cell populations and effector molecules theorised to be involved in the protective immune response to BCG. Peripheral blood samples collected from neonates prior to BCG vaccination, as well as 2-3 days, 1-2 months and 6-7 month after vaccination will be analysed using the flow cytometry panel as well as being subject to RNA sequencing. Studying the immune response to BCG in neonates, who exhibit the best response to BCG may further clarify how BCG induces immune memory.
Understanding the underlying immune mechanis d with BCG induced protection against Mtb strains could be key to developing the first novel vaccine since the development of BCG over 100 years ago.

Developing a Multisite Database for Background Rates of Adverse Events for Vaccine Evaluation in Africa

Luam Ghebreab[1], **Jennifer Griffin**[1], **Yannan Jiang**[1], **Kimberley Gutu**[2], **Jessica Ann Yun**[2], **Husna Ismail**[2], **Hazel Clothier**[1], **William Dormechele**[3], **Arier Lee**[1], **Clare L. Cutland**[2], **Jim Buttery**[1], **Steven B. Black**[1]
[1] Global Vaccine Data Network, Auckland, New Zealand, [2] Wits African Leadership in Vaccinology Expertise (Wits-Alive), School of Pathology, Faculty of Health Science, University of the Witwatersrand, Johannesburg, South Africa, [3] Navrongo Health Research Centre, Navrongo, Ghana

Background rates of adverse events following immunisation (AEFI) are critical for effective vaccine safety surveillance, enabling rapid detection and assessment of potential vaccine safety signals. However, such data are often lacking in low- and middle-income countries (LMICs), limiting the ability to conduct robust vaccine safety monitoring. The BRAVE (Background Rates for Adverse Events of Vaccination Evaluation) project ai to establish a harmonised, centralised database to collect and analyse baseline rates of AEFI across multiple sites in four African countries to strengthen vaccine safety monitoring in LMICs.

A secure REDCap (Research Electronic Data Capture) database was developed as the central repository linking all project sites to support harmonised data collection and management. REDCap was selected for its flexibility, scalability, and ability to support standardised, comparable data collection across diverse settings. The study protocol was translated into standardised electronic case report forms, site-specific data flows were designed, and both logical and physical database structures were implemented.
Development challenges included complex calculations and logic, variable internet connectivity, and diverse regulatory requirements. These were addressed through statistical software validation of complex rules, deployment of the REDCap mobile offline app, and tailoring workflows to site contexts while maintaining both local and international compliance standards. The BRAVE database enables centralised, real-time, quality-assured data collection and monitoring across all sites, ensuring standardised and comparable data for AEFI background rate estimation.

The BRAVE REDCap database demonstrates the feasibility and benefits of a harmonised, centralised data platform for managing complex, multisite vaccine safety studies in resource-limited African settings and offers a scalable model for strengthening global vaccine safety surveillance.

mRNA vaccine for protecting immunocompromised tamariki: a qualitative study of parents and caregivers' views

Leia Paltridge[1], **Amber Young**[2], **Cameron Burton**[1,3], **Simone Watkins**[1,4], **Kuang-Chih Hsiao**[1,5]
1 Department of Paediatrics: Child and Youth Health, University of Auckland, Auckland, New Zealand, 2 He Rau Kawakawa, School of Pharmacy, **Ōtākou** Whakaihu Waka, University of Otago, Dunedin, New Zealand, 3 Kidz First Children's Hospital, Te Whatu Ora Counties Manukau, Auckland, New Zealand, 4 Whangarei Hospital, Te Tai Tokerau Northland, Whangarei, New Zealand, 5 Department of Immunology, Starship Children's Hospital, Te Whatu Ora, Auckland, New Zealand

Immunocompromised tamariki and other vulnerable populations need protection against severe viral infections particularly during pandemics and community outbreaks. During the COVID-19 pandemic, the COVID-19 mRNA vaccine was broadly recommended by specialists to protect immunocompromised tamariki. For measles outbreaks, immunocompromised tamariki who cannot receive live viral vaccines heavily rely on community herd immunity to protect them. However, vaccine coverage is below the level needed for herd immunity against measles infection and alternative measures are needed to protect vulnerable tamariki.

The aim of this research is to understand whether Māori and Pacific parents/caregivers of immunocompromised tamariki would be willing to give their tamariki a non-live mRNA vaccine if available, to protect them against severe viral infections like measles.
This qualitative study investigated Māori and Pacific parents and caregivers' opinions on mRNA vaccines to protect their immunocompromised tamariki from measles infection in Aotearoa. Analysis was Kaupapa Māori-centered with an interpretive description methodology.

Ten parents/caregivers participated in this study. Seven were themselves vaccinated with mRNA vaccines against COVID-19. Three felt they had a good understanding of mRNA vaccines and seven said they would vaccinate their immunocompromised tamariki with a licensed mRNA vaccine against measles if available, with one participant being undecided about such vaccine. Further analysis was undertaken within a coding framework of the two main objectives. These were Opinions about mRNA vaccines to protect immunocompromised tamariki and To encourage uptake of a mRNA measles vaccine to protect immunocompromised tamariki. Within this framework, seven themes were derived from the data.

In conclusion, we identified that Māori and Pacific parents and caregivers of immunocompromised tamariki need to be well informed through multiple trusted sources and in a culturally appropriate manner before making decisions about mRNA vaccines. Furthermore, parents' and caregivers' concerns need to be identified and adequately addressed to ensure informed decision making.

Session 6

Data Sovereignty for Tāngata Whaikaha Māori: Insights from Te Ao Mārama Survey Panel

Andrew Sporle[1], **Taki Peeke**[2], **Tristram Ingham**[3], **Bernadette Jones**[3], **Meredith Perry**[3], **Paula Toko King**[3], **Barry Milne**[4]
1 iNZight Analytics Ltd, Auckland, New Zealand, 2 Te Ao Mārama Aotearoa Trust, Wellington, New Zealand, 3 University of Otago, Wellington, New Zealand, 4 University of Auckland, Auckland, New Zealand

Ensuring data sovereignty for tāngata whaikaha Māori is a Tiriti obligation and essential for equitable health and pandemic preparedness. The Te Ao Mārama Māori Health, Wellbeing, and Social Probabilistic Survey Panel is guided by Te Mana Raraunga principles, embedding Māori control over data governance, access, and use. Te Ao Mārama Aotearoa (TAMA) acts as kaitiaki, aligning with tikanga Māori and prioritising the rights and aspirations of tāngata whaikaha Māori.

The panel operates within a Māori Data Sovereignty Framework focusing on rangatiratanga (self-determination), whakapapa (relational accountability), and manaakitanga (beneficial for Māori communities). Governance is led by TAMA in partnership with cultural and scientific advisory groups, collaborating with the University of Otago to define ethical standards.
Using kaupapa Māori methodology and co-design, the study has revealed significant tensions between mainstream data infrastructure and Indigenous principles of collective governance, accessibility, and consent. Building trust with tāngata whaikaha Māori leaders has been crucial but resource-intensive. The framework has shifted research nor from deficit-based to strengths-based, whakapapa-informed narratives.

Key opportunities include embedding equity-by-design in survey infrastructure, enabling tāngata whaikaha Māori-led analysis, and future-proofing pandemic responses through inclusive, rights-based data governance. This demonstrates that true data sovereignty requires more than compliance; it necessitates transforming how data is conceptualised, governed, and used.

Te Ao Mārama provides a pathway for national syste to respect Indigenous data rights while improving resilience during health crises. Long-term panel studies are complex, requiring a balance between data continuity, institutional ownership, and Māori governance, cultural framing, and the obligations of kaitiakitanga.

Te Ao Māori Research Priority Theme: Whiitiki Whakatika

Raukura Roa, Raaniera Te Whata, Nanaia Mahuta, Huirama Matatahi
Tongikura Limited

Statement of the Problem: Whiitiki Whakatika addresses the challenge of enhancing pandemic resilience by examining how Mātauranga Māori historically and contemporaneously informed pandemic responses and preparedness among pā, kāinga, whānau, hapū and iwi across Aotearoa New Zealand. Drawing on the collective memory of devastating 19th and 20th century pandemics, the insights gained from learning from the past are critical for developing culturally responsive and self-determined strategies to address infectious disease threats.

Methods: Whiitiki Whakatika is a Kaupapa Māori led research project that undertook a qualitative and thematic analysis. Researchers collected data through wānanga (collaborative learning gatherings) and semi-structured individual interviews, engaging Māori experts, communities and organisations from across Aotearoa. The approach focused on capturing individual, collective and local narratives relating to pandemic responses, grounded in Mātauranga Māori principles.

Results: The analysis surfaced a rich tapestry of intergenerational survival strategies and self-determined health responses.

Key themes included:

- Historical narratives of Māori resilience
- Intergenerational knowledge transfer (kōrero tuku iho, pūrākau)
- Rangatiratanga (self-determination), proactive, and culturally anchored responses
- Future pandemic preparedness grounded in tikanga, whanaungatanga, manaakitanga, and rongoā Māori
- The importance of relational networks, kai sovereignty, mana motuhake / economic self-determination, spiritual wellbeing, and adaptive capacity at marae and within Māori organisations.

Significant Findings: The significant findings from this project demonstrate the enduring strength and resilience of te iwi Māori, grounded in tikanga and mātauranga Māori shaped our pandemic strategies. This project highlights how Māori communities leverage traditional values, relational networks, and adaptive practices to address infectious disease threats and challenges. The research further identifies key opportunities and challenges for integrating Māori values, practices, and governance into future emergency and health planning—ensuring that whānau, hapū, and iwi maintain agency over their own health and wellbeing.

Session 7 – Stream 1

Grounded in Community: Strengthening Pandemic Preparedness in Indigenous Communities

Fatima Ahmed[1], Eric Liberda[1], Nicholas Spence[1] & Nadia Charania[1]
1 University of Toronto, Toronto, Ontario, Canada

The Evaluating Pandemic Interventions in Indigenous communities (EPIC) project examined pandemic responses in two distinct Indigenous communities located in Ontario, Canada: Aamjiwnaang First Nation, an urban community, and Fort Albany First Nation, a remote community. Both communities had developed pandemic plans during the H1N1 outbreak, which were integrated with broader community management strategies. This project aimed to understand what worked well and what could be improved to strengthen future pandemic preparedness.

Using a community-based participatory research approach, we conducted semi-structured interviews with pandemic committee members and program leads directly involved in response efforts. This engagement provided a nuanced understanding of community experiences, revealing both successes and challenges. Key strengths included effective community-led coordination, culturally informed communication, and adaptive use of existing governance structures. Our findings highlight the value of grounding pandemic preparedness in local knowledge, community priorities, and culturally relevant frameworks. Aligning pre-existing community management plans with pandemic strategies enhances resilience and responsiveness, while tailoring interventions to specific geographic, social, and cultural contexts ensures equity and effectiveness.

Overall, the EPIC project demonstrates that participatory evaluation is a critical tool for improving pandemic responses in In-

digenous communities. By centering community voices and experiences, the project provides actionable lessons for strengthening preparedness, addressing structural barriers, and promoting health equity. These findings have broader implications for other Indigenous and marginalized communities seeking to build resilient, community-driven public health strategies.

Indigenous Leadership in Infectious Disease Preparedness: Integrating Sovereignty, Knowledge Systems, and Partnership

Eric Liberda[1], Fatima Ahmed, Nicholas Spence
1 Toronto Metropolitan University (Formerly Ryerson University), Toronto, Canada

Indigenous Peoples experience an unfair and unequal share of the negative health outcomes that flow from persistent and intergenerational inequities, environmental exposures, and colonial legacies. The priorities and leadership of Indigenous Peoples must be central to research on these health issues. This work offers a model for undertaking infectious disease research that is consistent with Ownership, Control, Access, and Possession (OCAP) principles, uses the Two-Eyed Seeing (Etuaptmumk) approach, and is based in Community-Based Participatory Research (CBPR).

OCAP principles enshrine collective data sovereignty: data about a Nation is owned, controlled, and stored by that Nation's custodians, such that cultural integrity can be protected, misuse minimised, and data used to benefit the community. The Two-Eyed Seeing framework, developed by Mi'kmaq Elders Albert and Murdena Marshall, advocates seeing the world through a lens that allows us to use the strengths of Indigenous knowledges and Western science in ethical spaces of engagement; spaces where reciprocity, co-learning, and mutual respect can inform infectious disease surveillance, prevention, and response. CBPR works to put these principles into practice, by ensuring community leadership throughout all stages of the research process: from setting priorities and developing questions to data interpretation and knowledge translation.

In this talk, we will explore the potential learnings and synergies these approaches have with Kaupapa Māori research to address health inequities particularly in relation to improving pandemic and emerging infectious disease preparedness. By embedding Indigenous leadership and authority within surveillance and response systems, these approaches can help ensure that culturally grounded communication and engagement strategies are developed and that public health interventions align with Māori aspirations for self-determination. This not only strengthens capability but also advances equitable health outcomes and preparedness for both Indigenous and non-Indigenous populations in the face of current and future infectious disease threats.

Migration Health Initiative: From Emergency Response to Global Health Equity

Md William Stauffer[1], Erin Mann, Syreeta Wilkins
1 University of Minnesota, Minneapolis, United States

The Migration Health Initiative was initiated as the National Resource Center for Refugees, Immigrants and Migrants (NRC-RIM) as the main United States response to COVID-19 in RIM populations. MHI promotes health equity and is uniquely designed for emergency preparedness and response in RIM communities, locally and globally, utilizing gold-standard best practices in health education, community engagement, and human-centered design.

Born from the urgent need to address health disparities during the COVID-19 pandemic, MHI rapidly transformed from an innovative emergency response concept into a nationally recognized organization excelling in public health emergency preparedness and fostering meaningful community partnerships. MHI specializes in creating community-participatory and informed, cultural and linguistically appropriate and timely health information and toolkits for capacity building for global implementation across community-based organizations, governmental agencies, NGOs, and Ministries of Health. MHI's impact demonstrates the scalability of community-centered pandemic response models.

In 2024 alone, the initiative reached over 71,000 unique website visitors from 183 countries, providing culturally validated resources in 40+ languages. The organization has developed 36 health education campaigns covering critical areas including maternal child health, infectious diseases, mental health, and nutrition. Through partnerships like the collaboration with the International Rescue Committee, MHI's Afghan health promotion efforts reached 3,842 people nationwide, while workforce development initiatives with the UN Migration Agency included 36 in-person trainings across 13 countries.

The model addresses the dual challenge of supporting over 123 million forcibly displaced people worldwide while alleviating pressure on underfunded organizations through cost-free resources and centralized services. MHI's approach seeks to reduce cost while increasing quality, decreasing research duplication, and offers replicable program templates to leverage maximizing limited resources.

This presentation will introduce MHI, demonstrating the critical intersection of pandemic preparedness and migration health in building resilient communities worldwide.

Inclusive preparedness: Strengthening pandemic plans for migrant and refugee communities

Nadia Charania[1]
1 Auckland University of Technology, Auckland Central, New Zealand

Aotearoa New Zealand accepts migrants and refugees under various pathways, with migrants now representing over a quarter of the total population. During the COVID-19 pandemic, migrant and refugee background communities were disproportionately impacted as infectious disease outbreaks can amplify pre-existing inequities. To improve health outcomes and better protect migrants and refugees during future pandemics, it is imperative to understand the complex, dynamic factors that are at play over the phases of a pandemic from the perspectives of migrants and refugees. Complexity science takes a strengths-based approach and offers a promising framework for investigating the inherent complexity within syste and the influence of wider interacting societal forces.
This multi-phase research programme harnessed the principles of complexity science to improve pandemic prevention, preparedness, and response, focusing on migrants and refugees who are often overlooked in preparedness efforts. Guided by an interpretive description methodology, narratives were qualitatively collected from semi-structured interviews and focus groups with multiple stakeholders. This included community members (n=7), organisation leaders (n=5), and pandemic planners (n=17). Data was analysed using a directed qualitative content analytic approach to produce visuals that crystallised the interconnected actors and factors.

Preliminary findings indicate that the specific needs of migrant and refugee background communities were overlooked in pandemic plans and the response. However, participants spoke to how relationships were leveraged at multiple levels to support community members, and the various strengths and resources present within communities. Participants called for a voice in pandemic planning, more support for community-based leadership, and concerted efforts to address the root causes of health inequities. It is anticipated that the outcomes of this research programme will inform improvements to pandemic preparedness plans to better address the needs of migrants and refugees during future pandemics.

Antimicrobial resistance and ecosystem health surveillance in freshwater environments

Rose Collis[1], **Arapera Paewai**[2], **Penelope Drysdale**[3], **Hone Morris**[4], **Amy Gault**[5], **Shaun Wilkinson**[5], **Adrian Cookson**[1]
1 AgResearch, Bioeconomy Science Institute, Palmerston North, New Zealand, 2 Taiao Ora Contracting, Dannevirke, New Zealand, 3 Te Miro Farm, Drysdale Dairies, Norsewood, New Zealand, 4 Te Kunenga ki Pūrehuroa, Massey University, Palmerston North, New Zealand, 5 Wilderlab NZ Limited, Wellington, New Zealand

Antimicrobial resistance (AMR) is a burden for human, animal and environmental health. In Aotearoa, New Zealand (NZ), efforts have focused on promoting antimicrobial stewardship, and community prescription of antimicrobials has been decreasing in NZ since 2015, but there is still relatively high usage of antimicrobials in human medicine, with the number of antimicrobial resistant pathogens increasing. In contrast, NZ is a relatively low user of antimicrobials in food-producing animals, with low rates of A in bacteria from food animals. Despite being part of the One Health triad, little is known about A in the environment in NZ. Further research is required to understand the role of the natural environment in A transmission. This research project ai to investigate innovative methods for A surveillance in the environment and will assess the use of freshwater and māwhaiwhai (spider webs) for monitoring ecosystem biodiversity and A in the NZ environment at sites d with contrasting land-uses.

Freshwater and māwhaiwhai samples were collected from three sites with contrasting land-uses: urban, agricultural and a reserve. Environmental samples were enriched and screened for extended-spectrum μ-lactamase (ESBL)-producing Enterobacteriaceae, with presumptive ESBL producers only isolated from urban freshwater samples. DNA was extracted from the samples and enrichments, and long-read Nanopore metagenomic sequencing is being utilised to characterise microbial communities, detect pathogens, and identify A genes. In parallel, environmental DNA analysis of māwhaiwhai and freshwater samples was undertaken to assess biodiversity and ecosystem health at the sample sites.

This research investigates A and biodiversity in freshwater and māwhaiwhai samples across sites with contrasting land-uses, combining A surveillance with environmental DNA monitoring. By integrating māwhaiwhai and freshwater into existing surveillance frameworks, we aim to enhance our understanding of ecosystem health and A in the environment and contribute to better strategies for mitigating the transmission of AMR.

Harnessing the antiviral activities in Pacific traditional medicines

Natalie Netzler[1,5], VH Woolner[1,3], S Molimau-Samasoni[2], Robert Keyzers[3], Vernon Ward[1,4]
1 Maurice Wilkins Centre of Research Excellence, Auckland, New Zealand, 2 Scientific Research Organisation of Samoa (SROS), Apia, , Samoa, 3 Victoria University of Wellington, Wellington, New Zealand, 4 University of Otago, Dunedin, New Zealand, 5 Waipapa Taumata Rau | University of Auckland, Grafton, Auckland, New Zealand

We lack specific antivirals and vaccines to combat most viral pathogens, and for some global regions these few therapeutic solutions are inaccessible. We urgently need additional safe and effective antivirals to protect all communities, especially those with co-morbidities which can contraindicate clinically approved antivirals such as Paxlovid. Crucially, many Pacific villages and remote communities face significant barriers to medical care, with no easy access to hospitals, doctors or medical clinics without taking a flight or boat to another region. For these populations, easily accessible, affordable, safe and trusted antiviral therapies are urgently needed.

Over many centuries, Pacific populations have developed and administered effective traditional medicines to treat a range of illnesses. Several Pacific traditional medicines have been shown to possess potent anti-inflammatory and antimicrobial properties, however, very few studies have directly examined their antiviral effects against current viral threats such as COVID-19. This study examined a range of traditional Samoan medicines for antiviral activities against pathogenic viruses including SARS-CoV-2, RSV and herpes simplex virus, using gold standard virological assays. For traditional medicines demonstrating antiviral properties, we further examined these in combinations with other traditional medicines or clinically approved antivirals to look for therapeutic synergy, which allows for dose reductions of each therapy, but can also detect antagonism to guide appropriate use. Our results revealed two Samoan traditional medicines with potent antiviral activity against the SARS-CoV-2 Omicron variant and broad-spectrum activity against other diverse viruses including RSV and herpes, with one showing synergistic activity when combined with the clinical antiviral Nirmatrelvir.

This study combines the complementary expertise from traditional medicine practitioners and Pacific researchers to enhance indigenous knowledge and to work with traditional healers to help combat contemporary viral infections in remote areas.

Rejuvenating the ageing immune system to improve vaccine efficacy in older people

Theresa Pankhurst[1,2], Rebecca McKenzie[1], Michelle Linterman[1]
1 Malaghan Institute of Medical Research, Wellington, New Zealand, 2 Babraham Institute, Cambridge, United Kingdom

Our global ageing population faces unique challenges in achieving protective immunity following vaccination. Immunosenescence refers to the age-related decline in immune function and poses a significant barrier to effective vaccination among older adults worldwide. For us in Aotearoa NZ, safeguarding kaumātua and kuia is both a scientific and cultural imperative. Our kaumātua are the keepers of mātauranga Māori, whakapapa, and tikanga; their wellbeing underpins the health of the collective and the continuity of intergenerational knowledge.

Our research addresses this challenge by establishing a targeted preclinical testing pipeline to evaluate vaccine strategies for ageing immune systems. Using young and aged mice, we investigate the impact of age on antibody production, germinal centre responses, and immune cell activation that are critical components of vaccine-mediated protection. Our work reveals that aged mice show delayed and impaired vaccine responses, leading to diminished protective immunity compared to younger adult mice.
Within an Aotearoa NZ-UK research partnership, we are using our established preclinical pipeline to test novel influenza mRNA vaccines hypothesized to restore function to the aged immune system. This work ai to support the development of vaccines specifically tailored to older immune systems, ultimately enhancing protection for those who are both most vulnerable to infectious diseases, and most deeply valued within whānau Māori.

Mini-lungs as an airway disease model platform

Andrew Highton[1], Roslyn Kemp[1], Jack Dummer[2]
1 Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand, 2 Department of Medicine, University of Otago, Dunedin, New Zealand

Respiratory infections are responsible for over 5% of global mortality, and new technologies are urgently needed to monitor and reduce this burden. Mini-lungs (airway organoids) are an advanced 3D cell model system that allow for study of the lung

in a lab setting. Mini-lungs are derived from primary cells donated by patients from bronchoalveolar lavage fluid or surgery resections, so are highly representative of individual patients, positioning them as a powerful tool for personalised medical applications. It is also possible to infect mini-lungs with viruses such as SARS-CoV-2 (causing COVID19), influenza, and those that cause common colds, such as rhinovirus. These features position mini-lungs as a unique and valuable system to study existing and emerging viral threats.

The immune system is the most important defence against viral infection and it is therefore important to understand how immune cells respond to viral challenge. Of particular importance early in viral infection are cytotoxic immune cells, including CD8 T cells and natural killer cells as these cell types are able to directly kill cells infected with virus and produce inflammatory cytokines. It is important to understand immune responses to different viruses, and how those responses can be enhanced to provide enhanced protection for patients. Here, we establish a co-culture system of mini-lungs and natural killer cells to create an accurate lung disease model system in the lab. Mini-lungs consisted of the expected differentiated cells. It was demonstrated that differing cytokine iles had could alter mini-lung growth and these development characteristics could be effectively monitored using machine visions and microscopy.

Altogether, this technology could provide a vital platform for rapid monitoring of emerging viral threats and to understand the immune component of viral defence in lung infections.

Session 7 – Stream 2

A population-based study of hospitalisation for acute gastroenteric infection in Aotearoa New Zealand (2010–2019)

Alice Hyun Min Kim[1], James Stanley[1], Ross Ihaka[2], Tim Chambers[3], Farnaz Pourzand[1], Sharla McTavish[1], June Atkinson[1], Michael Baker[1], Simon Hales[1]
1 Ōtākou Whakaihu Waka - University of Otago, Wellington, New Zealand, 2 Waipapa Taumata Rau - University of Auckland, Auckland, New Zealand, 3 Te Whare Wānanga o Waitaha - University of Canterbury, Christchurch, New Zealand

Acute gastroenteric infection (AGI) is preventable, yet it is globally and nationally d with a significant burden of disease. Young children and older age groups are especially at high risk of infection and hospitalisation. NZ has high rates of AGI by international standards. Furthermore, in Aotearoa, the case rates are inequitably distributed based on land use and neighbourhood socioeconomic status. For example, communities relying on untreated private water supplies or living in rural agricultural areas face elevated risks. Variations in rainfall and ambient temperature can also influence the risk of AGI. Less is known about the influence of these factors on hospitalisation rates.

We conducted a population-based study of hospitalisation rates for AGI from 2010 to 2019. The crude rates for total hospitalisation confirmed the differences in rates based on age, for example, with children under 5 having 3.6 (95% CI: 3.55, 3.65) times the rate of adults aged 20-39 years. Age-standardised rates showed dose-response disparity by neighbourhood deprivation. The areas with the highest deprivation scores had double the rate of areas with the lowest deprivation scores. Hospitalisation risks were heightened during Spring (from September to November) compared to other months.

The age-standardised rates linked to key specific pathogens such as Campylobacter, Salmonella and Rotavirus showed distinct annual trends over 2010-2019. Rates by ethnicity also differed by pathogen[s], with the Sole European group showing the highest rate for campylobacteriosis. However, all ethnic groups showed high rates of hospitalisation for which a specific pathogen or agent was not identified.

Hospitalisation for acute gastroenteric infections has unequal distributions by area deprivation and demographic factors. Future analyses will focus on the impact of high-density dairy cattle farming, heavy rainfall and poor water quality on the risk of hospitalisation.

Drinking water quality and enteric disease: a nationwide case-crossover study (2015–2019) in New Zealand

Tim Chambers[1], Simon Hales[2], Farnaz Pourzand[2]
1 University of Canterbury, Christchurch, New Zealand, 2 University of Otago, Wellington, New Zealand

Background: Despite the well-known effects of microbiological contamination of drinking water on enteric disease, there is limited epidemiological research investigating the relationship with drinking water quality determinands.

Objective: To investigate the association between drinking water determinands and enteric disease

Methods: This study used a nationwide case-crossover study design of 46,020 cases of enteric disease between 2015 and 2019. Cases were successfully linked to a public water supply and exposure to E. coli, total coliforms, turbidity and free available chlorine quantified for case and control periods.

Results: There were no statistically significant associations found between all enteric, bacterial only, or protozoan only enteric disease notifications and water quality determinands. The presence of E. coli was d with increased risk of enteric disease in supplies served by surface water (OR 1.23: 95%CI 1.04, 1.46), with known source water risks (OR 1.28: 95%CI 1.08, 1.52) and where the case was exposed to the highest tertile of rainfall (OR 1.27: 95%CI 1.01, 1.58).
Significance: Major outbreaks of enteric disease can be caused by contamination of public drinking water supplies. Our findings suggest that this mechanism might also be responsible for sporadic cases of enteric disease caused by zoonotic bacterial pathogens.

Association between heavy rainfall, dairy cattle density and campylobacteriosis (2015–2019)

Simon Hales[1], Tim Chambers[2], Farnaz Pourzand[1], Alice Kim[1], Michael Baker[1]
1 University of Otago, Wellington, New Zealand, 2 University of Canterbury, Christchurch, New Zealand

Studies have attributed outbreaks of enteric disease to heavy rainfall events. In Havelock North, in 2016, heavy rainfall caused contamination of a water supply by livestock faeces, leading to a major outbreak of campylobacteriosis. Drinking water supplies served by groundwater are better protected against microbial contamination than surface water, but the presence of livestock has been linked with enteric disease. Here we investigate short-term associations between rainfall, dairy cattle density and notifications of sporadic campylobacteriosis.

We fitted conditional Poisson regression models in a space-time stratified case-crossover study design. Daily notifications of campylobacter by 2018 meshblock code were obtained from the national surveillance system (2015-2019); 26,436 (79%) were geocoded to a water distribution zone (WDZ).

Rainfall and maximum temperature from the NIWA Virtual Climate Station Network were averaged averaged over 7-day lag periods within 10km circular buffer zones centred on WDZ source abstraction points. Dairy cattle density for the same areas were estimated using meshblock data for 2018 from Agribase. Final models were stratified by quintiles of dairy cattle density.
Among WDZ with the lowest quintile of dairy cattle density (zero cows/km^2), there was an increased risk of campylobacter in the 10th decile of 7-day average lagged rainfall: IRR 1.11 (95%CI: 1.02-1.22). In the upper quintile of dairy cattle density (~150 cows/km^2) there was an increased risk of campylobacter in the 6th to 10th deciles of rainfall, with a dose-response relationship. This association was strengthened in WDZ using surface water sources: for example, IRR 1.69 (1.27-2.24) for the 10th decile of rainfall.
The risk of sporadic campylobacteriosis was significantly d with heavy rainfall in the 7 days prior to disease onset, especially in locations served by surface water supplies with a high density of dairy cows within 10km from the source. This is probably related to contamination of the source water.

Spatial Modeling of Campylobacteriosis Notification Rates in Relation to Drinking Water Supply Characteristics

Farnaz Pourzand[1], Alice H.M. Kim[1], Tim Chambers[2], Leah Grout[3], Michael G. Baker[1], Simon Hales[1]
1 University of Otago, Wellington, New Zealand, 2 University of Canterbury, Christchurch, New Zealand, 3 Southern California University of Health Sciences, Whittier, CA, USA

Campylobacteriosis, a leading cause of bacterial gastroenteritis in New Zealand, is traditionally d with contaminated poultry consumption. However, drinking water, particularly from private supplies, has emerged as a significant source of infection. Private water supplies, which remain largely unregulated under the Water Services Act 2021, can contribute to disease outbreaks, especially in rural areas. This study investigates the relationship between water supply characteristics and Campylobacteriosis notification rates from 2015 to 2019. Cross-sectional Poisson regression models were used to assess the impact of water supply type, rurality, livestock density, and extreme weather events on Campylobacteriosis rates. Data were analyzed for the years 2015 to 2019, focusing on rural areas with varying dairy farm densities. Our results indicate that private water supplies in rural areas with high dairy cattle density were significantly d with increased campylobacteriosis rates (Relative Risk (RR) = 2.21, 95% CI: 1.60-3.05) compared to urban areas with public water supplies. We also observed a significant positive association between dairy cattle density and increased campylobacteriosis incidence in private rural water supplies. Low dairy density is d with an 18% higher risk (RR = 1.18, 95% CI: 1.04-1.34), medium density with a 17% higher risk (RR = 1.17, 95% CI: 1.03-1.33), and high density with a 47% higher risk (RR = 1.47, 95% CI: 1.28-1.69) compared to areas with no dairy cattle. These findings underscore the significant role of private water supplies in rural areas, especially where intensive dairy farming is prevalent. They highlight the urgent need for improved water quality management and monitoring in rural regions to reduce campylobacteriosis risk. Our study has

critical implications for public health policy, particularly in supporting rural communities reliant on private water systems, and contributes to the broader understanding of environmental risk factors in infectious disease transmission.

Emerging Campylobacter species linked to human diseases at a wildlife–livestock–human interface in Uganda

Valter Almeida[1], Matthew A. Knox[1], Kim M. Handley[2], Anne C. Midwinter[1], Patrick J. Biggs[1], Agata H. Dziegiel[3], Gladys Kalema-Zikusoka[4], Stephen Rubanga[4], Alex Ngabirano[5], Willy A. Valdivia-Granda[6], Hayley MacGregor[7], Nigel P. French[1], Alison E. Mather[3], James O. Lloyd-Smith[8], David T. S. Hayman[1]
1 Massey University, Palmerston North, Manawatū-Whanganui, New Zealand, 2 University of Auckland, Auckland, New Zealand, 3 Quadram Institute Bioscience, Norwich, Norfolk, United Kingdom, 4 Conservation Through Public Health (CTPH), Buhoma Village, Kanungu District, Uganda, 5 Mubare Biodiversity Conservation (MBC), Kanungu District, Kanungu, Uganda, 6 Orion Integrated Biosciences, Inc., Manhattan, Kansas, United States of America, 7 University of Sussex, Brighton, East Sussex, United Kingdom, 8 University of California, Los Angeles, California, United States of America

Campylobacter species are leading causes of bacterial gastroenteritis worldwide, yet their diversity and transmission at wildlife–livestock–human interfaces remain poorly characterised. We investigated Campylobacter diversity across sympatric mountain gorillas, livestock, and humans in Buhoma, Uganda, and assessed its clinical relevance in human samples.
We analysed 553 faecal samples from mountain gorillas (n=200), cattle (n=83), goats (n=73), and humans (n=197). DNA was extracted and subjected to Illumina shotgun sequencing. Metagenome-assembled genomes (MAGs) were reconstructed, dereplicated, and taxonomically classified using GTDB-Tk. Phylogenetic and functional analyses were conducted, and Campylobacter abundance compared across host groups. Associations with human disease were evaluated through read-based mapping and statistical analysis in R.

We recovered 44 Campylobacter MAGs representing seven species, including five putative novel taxa. Mountain gorillas harboured three of these novel species, while livestock carried C. vicugnae (goats) and C. sp017646085 (cattle). Human gut microbiomes contained Candidatus Campylobacter infans, which was not d with disease, and C. sp900539255, which was significantly enriched in clinical samples (p=0·001). Functional iling revealed unique sulphur and nitrogen metabolic pathways and a gene encoding a GH73-family glycoside hydrolase in C. sp900539255. Antimicrobial resistance genes, including bla-OXA-471_1, were detected in Ca. C. infans MAGs.

Our findings reveal high Campylobacter diversity at the human–animal interface in Buhoma, including novel species with potential relevance to human health. The significant association of C. sp900539255 with clinical samples highlights the need for improved surveillance of emerging Campylobacter species. Expanding genomic reference databases is essential for accurate detection, characterisation, and monitoring of pathogenic lineages to support public health interventions in zoonotic hotspots.
Funding: Royal Society Te Apārangi, Percival Carmine Chair in Epidemiology and Public Health, Massey University.

Session 8 – Stream 1

Infectious disease modelling to support communities

Sarah Pirikahu[1], Amanda Kvalsvig, Michael Baker, Noella Taiapa, Temi Allinson, Katrina Ford, Tia Dawes
1 University of Otago, Wellington, New Zealand

Infectious disease modelling plays a critical role in informing public health decision-making. Centering these efforts on the priorities of whānau within our community strengthens the relevance and impact of these modelling efforts. The aim of this project is to identify how disease modelling can address the infectious disease priorities of Māori communities and how surveillance syste need to be enhanced to support this mahi. Methods: We engaged with public health experts, Māori health providers and their whānau using semi-structured interviews to understand their infectious disease priorities and aspirations for infectious disease prevention, control and surveillance. Alongside our community engagement we conducted a review of the respiratory infectious disease mathematical modelling landscape in Aotearoa to identify current gaps and opportunities. Results: Our review highlighted a large volume of mathematical modelling related to COVID-19 in Aotearoa, with limited work on other respiratory infections. Notably, no mathematical studies were found regarding bacterial infections, and RSV and pertussis were significantly under-represented despite their public health significance. Our community engagements highlighted that whānau conceptualise health and illness more holistically and the pressures d with cost of living and immediate health needs take priority over infectious diseases. Childhood infectious diseases and seasonal flu, however, were identified as a common concern across groups. Amongst Māori health providers and public health experts there is a shared aspiration for our surveillance syste to be more accessible, to provide more granular data, to support bi-directional information sharing and to better align with Te Ao Māori and a collective, whānau-centered approach. Conclusion: There is considerable opportunity to

utilize mathematical modelling, aligned with the infectious disease concerns of Māori, to generate evidence which supports public health response. A shift towards a surveillance system that integrates whānau-level data also opens-up the possibility for modeling that better reflects disease transmission dynamics and social mixing.

Microbial cell-free DNA: a non-invasive approach to diagnosing infectious diseases

Amy Scott-Thomas[1], Masuma Zawari[1], Elizabeth Chernysheva[1], Katie Wolf[1], Trevor Anderson[2], Allison Miller[1], Michael Maze[3], Malina Storer[4], Martin Kennedy[1], Nicholas Douglas[3], Allamanda Faatoese[5], Stephen Chambers[1]
1 Department of Pathology and Biomedical Sciences, University Of Otago, Christchurch, Canterbury, New Zealand, 2 Canterbury Health Laboratories, Christchurch, Canterbury, New Zealand, 3 Department of Medicine, University of Otago, Christchurch, Canterbury, New Zealand, 4 Canterbury Respiratory Research Group, Canterbury District Health Board, Christchurch, Canterbury, New Zealand, 5 Christchurch Heart Institute, University of Otago, Christchurch, Canterbury, New Zealand

Introduction: Diagnosing infectious diseases is often difficult, especially when the pathogen is slow-growing, hard to culture, or requires invasive sampling. Our goal was to develop two diagnostic platfor to detect microbial cell-free DNA (mcfDNA) in patient urine and blood. These assays would allow rapid, non-invasive diagnosis of diseases such as Legionnaires' disease and Kingella kingae infections in tamariki. Both platfor were designed to be adaptable, so they can detect any pathogen with a sequenced genome, making them useful for a wide range of hard-to-diagnose infections.

Methods: We developed two complementary approaches. The first used a hybridisation assay with pathogen-specific probes to capture and detect Legionella DNA fragments in urine. The second method employed a CRISPR-Cas12a system for sequence-specific recognition of Legionella DNA extracted from blood, coupled with a reporter assay for rapid signal generation. Both were optimised for high sensitivity and specificity, enabling the detection of low concentrations of mcfDNA from non-invasive samples.

Results: The hybridisation assay reached 100% specificity and 90% sensitivity, outperforming a commercial kit and phenol–chloroform DNA extraction. The CRISPR-Cas12a assay showed 100% specificity and sensitivity down to one genome copy per assay. Clinical validation of both assays using urine and blood samples is now in progress.

Conclusion: Both assays show strong performance for detecting Legionella cfDNA and are being utilised for other pathogens. The hybridisation platform has been modified for the detection for Kingella kingae infections, while the CRISPR-Cas12a system has been adapted for Mycobacterium leprae. These results show the flexibility of the mcfDNA platforms. The development of these assays has solidified collaborations with clinical microbiologists and clinicians while supporting the development of new connections with Māori and Pasifika health partners and international researchers, moving us closer to clinical use and building capacity for infectious disease diagnostics in Aotearoa New Zealand.

Point-of-use testing for infectious diseases in the community

Shirley Keown[2], Craig Billington[1], Glenda Raumati[3], Rachel Fleming[4]
1 PHF Science, Christchurch, New Zealand, 2 Turanga Health, Gisborne, New Zealand, 3 Ngā Miro Health, Ngaaruawaahia, New Zealand, 4 PHF Science, Auckland, New Zealand

In this project, we are responding to the Te Niwha mission by building research capability for Aotearoa in rapid point-of-use molecular diagnostics for future infectious disease challenges. COVID-19 has taught us that there are significant inequities in access to healthcare which may be a result of cultural, economic or geographic factors (or all three). Shifting the detection of diseases from the laboratory or hospital to on-site testing in communities allows individuals and communities to take control of their own health and environmental resources and better prepares the whole of Aotearoa to monitor and respond to future pandemics or other disease challenges. Using the principles of tūhonotanaga and hononga, we have formed collaborations with Turanga Health (Te Hauora o Turanganui a Kiwa) and Ngā Miro Health (Ngā Miro Charitable Trust) to work in partnership with their communities to ensure their needs and aspirations are central to the research. We listened to community concerns and identified their two highest priority assays: Group A streptococcus and RSV. We have designed these new assays along with a mobile phone app to record results. The final phase for the project is refining hardware and data science (including data sovereignty and security and other cultural considerations) and testing sample collection and assay workflows.

Point-of-care testing paired with cervical screening pathways: a study of healthcare delivery in remote Aotearoa

Jo-Ann Stanton[1], Bev Lawton[1], Ngaire Sparkes[1], Kia Paasi[1], Jane McDonald[1], Francesca Storey[1], Marion Saville[2], David Hawkes[2], Stacie Geller[3], Melanie Gibson[1], Anna Adcock[1], Merilyn Hibma[4], Mathew Bennett[1], Charles Lambert[1], Peter Sykes[5], Huti Watson[6], Gina Chaffey-Aupouri[6], Helayna Reedy[6], Mel Ratapu[6]
1 Te Tātai Hauora o Hine, Victoria University Wellington, Wellington, New Zealand, 2 Australian Centre for the Prevention of Cervical Cancer, Carlton, Victoria 3053, Australia, 3 Obstetrics and Gynecology, University of Illinois College of Medicine, Chicago, Illinois, United States of America, 4 Department of Pathology, University of Otago, Dunedin, Otago, New Zealand, 5 Department of Obstetrics and Gynaecology, University of Otago, Christchurch, Canterbury, New Zealand, 6 Ngāti Porou Oranga, Te Puia Springs, Tairawhiti, New Zealand, 7 Queen Street Practice, Wairoa, , New Zealand, 8 National Institute for Health Innovation, University of Auckland, Auckland, New Zealand

Background: This study posed the question 'Can a community controlled cervical screening pathway paired with PoCT lead to timelier colposcopy for treatment of pre-cancerous cervical lesions?' We developed a health delivery model that empowered local communities and then measured timeliness of test-to-colposcopy when referred from rural practices.

Methods: We undertook a 30-month cluster-randomised crossover trial involving 1,410 participants (PoCT arm = 632, standard care arm = 788). Three remote rural clinics were established that performed HPV-based point-of-care screening using the Cepheid GeneXpert IV. Compliance with New Zealand Best Practice Guidelines for PoCT ensured safe services were provided to patients. Clinics undertaking HPV-screening at point-of-care required minimal site modification, and appropriate staff training, quality assurance and iciency progra before service implementation.

Results: High-risk HPV was detected in 125 participants. Women with a positive HPV result were 4.7 times more likely to attend colposcopy within 20 working days of the test results when PoCT was part of the community-controlled healthcare pathway (odds ratio: 4.7, 95% confidence interval: 1.7 to 12.8). Healthcare providers found offer of PoCT within a community-controlled pathway was acceptable. Qualitative interviews showed providers reported being able to build greater rapport with patients and could place women on an appropriate treatment pathway more quickly. Significantly, continuous provision of healthcare was possible during the COVID pandemic and through natural disasters.

Conclusion: This research demonstrates the value of PoCT to rural models of care in Aotearoa New Zealand. Utilizing this technology within an appropriate clinical pathway can potentially aid diagnosis, facilitate timely treatment and improve health outcomes even during times of crisis. It has informed new PoCT studies underway, exploring whānau-centred diagnostic testing and development and adaptation of appropriate and sustainable care pathways concerning respiratory, skin and other infections. These findings may be applicable to other communities in high-income countries.

Co-development of regional specific frameworks for exploring new anti-microbial and anti-viral agents sourced from taonga herbal remedies

Joanne Murray, Wayne Blissett, Isabel Moller, Dominic Lomiwes, Nayer Ngametua, Moana Hamana, Melanie miller, Renata Blissett, Jonni Koia
1 Te Hiku Rongoā collective, Rangitāne o Manawatū, 2 Tuia te Oranga Best Care (Whakapai Hauora), 3 The New Zealand Bioeconomy Science Institute

Aotearoa New Zealand's indigenous flora is one of the most unique and diverse in the world. Many species of taonga flora are rongoā that have medicinal properties used by Māori for hundreds of years providing relief for many common ailments and chronic conditions over centuries.

Here we will discuss the co-development of regionally specific framework(s) by Rangitāne o Manuwatū and Te Hiku Rongoā collective in partnership with researchers to guide the sourcing, harvesting, processing and scientific analysis of rongoa rākau. We discuss scientific approaches and d ethical and data sovereignty considerations as well as risk and benefits of the proposed research. Importantly, we demonstrate how scientific knowledge can be used affirm existing mātauranga and work alongside rongoā mātauranga to inform its use.

We further outline how these frameworks will be applied to scientific approaches being to understand anti-microbial, anti-viral and immune modulatory effects of rongoā rākau.

Pacific Cultural Best Practice Approach results to 100% Pacific Participants in Carriage Study

Galumalemana Vaifagaloa Naseri[1]
1 Pasefika Family Health Group Ltd., Glendene, New Zealand
Use of the Culturally Best Practice Approach to Engage and Recruit Pacific Households to Participate in the Carriage Study in South Auckland.

Background: The Pasefika Family Group partnered with the University of Otago and New Zealand Institute of Public Health and Forensic Science, to conduct a carriage study of pneumococcus and meningococcus in Pacific households in South Auckland. Applying Pacific cultural best practices effectively recruited Pacific families and the community to participate in the study. No family withdrew from participation.

Methods: To recruit eligible participants, households were selected from the Pasefika Family Health Group database, and through outreach and community engagement processes. Families were contacted by phone to request an in-person meeting about the project. All communication was conducted in the families preferred first language or English. Essential Pacific values such as respect, humility, and reciprocity, were consistently observed. Families determined appointment times for swabbing, allowing them to set the schedule according to their preferences. Most swabbing sessions occurred after hours or during weekends when all family members were available. Field workers were often invited to share a cup of tea or meal- a Pacific tradition reflecting hospitality and love. (Alofa). Throughout the study, our approach was engaging the family as a partner, allowing them to lead their own schedule, which further fostered trusting relationship and collaboration.

Findings: Through open discussion and observation, the team enhanced families understanding of health, wellbeing and disease, including pneumococcus and meningococcus. Families developed strong trust in the team, fostering relationships that will facilitate future participation and wider community engagement.

Significance: Pacific families often experience consultation fatigue and are always reluctant to engage with health and public service workers. A culturally informed approach to relationship building can support future engagement.

Community-Led Approaches to Carriage Surveillance of Infectious Diseases in Te Hiku o Te Ika

Conor O'Sullivan[1], **Te Aumihi Jones**[1], **Xiaoyun Ren**[2], **Phillip Hill**[3], **Mishal Manisha**[3]
1 The Moko Foundation, Kaitaia, New Zealand, 2 Health, PHF Science, Wellington, New Zealand, 3 Centre for International Health, University of Otago, Dunedin, New Zealand

Invasive meningococcal and pneumococcal diseases disproportionately affect Māori and Pacific communities, especially tamariki and kaumātua. While Aotearoa has strong surveillance of invasive disease, little is known about the asymptomatic carriage of Neisseria meningitidis and Streptococcus pneumoniae. We are part of a broader Te Niwha funded project delivering a community-based carriage study for meningococci and pneumococci within households in regions of high infectious disease prevalence.
Delivered through the Moko Foundation and Waharoa Ki Te Toi, this kaupapa represents an innovative approach to biomedical research, integrating scientific rigour with community participation and tikanga Māori. Engagement has gone beyond standard recruitment, involving consultation with a number of layers within the community, utilising key platfor such as a Marae and schools to ensure the research was tailored to the context of our rural Māori communities.

Laboratory components of the research have also been tikanga-informed, showcasing how effective partnership with maori can research spaces and scientists are enabled to uphold the tapu nature of biological samples. Standard methods such as surveys, swabbing, and data collection have been adapted using culturally safe protocols, enabling us to enact true kaitiakitanga and uphold Māori data sovereignty.

Beyond surveillance, this kaupapa prioritises education and building community awareness of infectious diseases and their transmission. Preliminary outcomes show high whānau engagement, improved health literacy, and strong support for Māori-led biomedical research.

This study demonstrates how Indigenous-led methodologies can enhance national disease surveillance while upholding tino rangatiratanga and fostering resilience in communities historically underserved by mainstream health systems.

Session 8 – Stream 2

Vibrio an emerging disease threat for Aotearoa: Hapū focus group findings

Maria Hepi[1], Mike Edmonds[2], Lucia Rivas[1], Eden Maikuku[2], Jasmine Teei[2], Sam Totten[2], Okeroa Waaka[2], Claudine Waitere[2], Wendy Dallas-Katoa[3], Peter Cressey[1], Nikki King[1], Lisa Lopez[1], Jackie Wright[1]
1 Phf Science, Christchurch, Canterbury, Aotearoa New Zealand, 2 Te Toi Ora ki Whaingaroa, Raglan, Waikato, Aotearoa New Zealand, 3 Independent Kaupapa Māori Researcher, Christchurch, Canterbury, Aotearoa New Zealand

Vibrio is a naturally occurring bacterium found in aquatic environments and is considered a microbial barometer for climate change. It can cause gastroenteritis or skin and tissue infections, ranging from mild to severe. In Aotearoa, outbreaks of Vibrio-related gastroenteritis have been linked to contaminated kaimoana, with Māori and Pacific Peoples (PP) disproportionately affected, potentially due to the practice of mahinga kai.

Vibrio thrives in warm water, so as climate change brings warmer ocean temperatures, conditions in which Vibrio thrives, there is a growing risk that exposure to Vibrio through kaimoana and mahinga kai will increase. This raises concerns about whether Aotearoa's current public health surveillance syste are adequate for monitoring these emerging risks, and whether they can be adapted to deliver more timely, culturally relevant public health messaging to Māori communities.

An analysis of available surveillance data revealed key gaps that limit accurate estimates of Vibrio illness burden. Māori and PP are overrepresented in Vibrio notifications (all clinical types) yet are underrepresented in notifications for other notifiable causes of acute gastroenteritis compared with other ethnic groups. This discrepancy signals a potential equity issue and suggests underestimation of disease burden, likely reflecting barriers to care and limited responsiveness of the health system.

To explore these issues further, 10 focus groups were held by Te Toi Ora ki Whāingaroa with hapū in the Waikato Harbour area. These focus groups gathered whānau experiences with gastroenteritis, skin infections, and primary care interactions. They also explored the role of community networks, mātauranga Māori , and practices such as rāhui when kaimoana is considered unsafe to collect. Insights from these kōrero may inform improvements in public health messaging. Co-analysis of the findings by PHF Science and Te Toi Ora ki Whāingaroa is scheduled for late August and will be shared at the upcoming Summit.

Leptospirosis in Aotearoa: climate-driven outbreaks

Shahista Nisa[1], Stuart Littlejohn, Ahmed Fayaz, Scarlet Deen, Maryna Sokolova, Paul Ogbuigwe, Marie Moinet, Adrian Cookson, Julie Collins-Emerson, Chris Niebuhr, Emilie Vallee, Jonathan Marshall, Jackie Benschop
[1] Massey University, Palmerston North, New Zealand

Leptospirosis disproportionally burdens rural and Māori communities in Aotearoa. In 2023, severe flooding was followed by a marked increase in human leptospirosis cases—an epidemiological pattern commonly observed overseas but previously unreported here. This prompted increased use of PCR-based diagnostics, decreasing serotyping information and limiting source attribution. Recent advances in molecular typing have enabled finer-scale associations between Leptospira strains and their host species, a method currently not in use by either human or animal diagnostic laboratories.

This study genotyped Leptospira DNA from human cases (2016–2023) using glmU amplicon sequencing and compared results with genotypes found in animals to infer potential sources of infection during the 2023 outbreak. Genotyping data were supplemented with national surveillance data, including serotyping results and regional distribution, to identify circulating serovars and outbreak locations. Statistical analyses (Chi-square and Poisson regression) were used to assess host–genotype associations, while phylogenetic analyses examined genetic relatedness among strains.

Flood- d outbreaks were identified in several regions. Genotyping results showed an increase in infections with a livestock- d strain (Leptospira interrogans serovar Pomona) in rural flood-affected regions (Gisborne, Hawke's Bay, Manawatū-Whanganui, Waikato and Wairarapa) in 2023 compared to 2016–2022. In animals, Pomona was primarily detected in sheep (Ovis aries), followed by cattle. In contrast, human cases from the Auckland region—which also experienced flooding—were predominantly d with wildlife- d strains: Leptospira borgpetersenii serovars Ballum and Balcanica_NZ, and Leptospira interrogans serovar Copenhageni. These strains were primarily detected in mice (Mus musculus), Norway rats (Rattus norvegicus), and brushtail possu (Trichosurus vulpecula), respectively.
This study highlights the need for integrating molecular diagnostics and animal surveillance into public health frameworks. As climate-driven weather events become more prevalent, zoonotic diseases may increasingly drive outbreaks. Strengthening One Health surveillance syste and genomic typing capacity is essential for early warning, targeted mitigation, and equitable preparedness strategies.

Para Hopuhopu – Wastewater Epidemiology

Maxine Graham[2], Sally Reid[3], Joanne Chapman[1], Brent Gilpin[1], Maatene Cooper[2], Rory Katipa[2], Tangiwai Katipa[2], Mere Komene[2], Ngaire Lasika[2], Dolly Paul[2], Brownie Rauwhero[2], Julie Wade[2], Jaysha Pompey[2], Lynn Lewis-Bevan[3], Keri Mills[5], Carla Eaton[1], Maria Hepi[1], Marama Muru-Lanning[4]
1 PHF Science, Christchurch, Canterbury, New Zealand, 2 Kei o te Waka o Tainui', Waikato, New Zealand, 3 Waikato-Tainui College for Research and Development, Ngāruawāhia, New Zealand, 4 University of Auckland, Auckland, New Zealand, 5 Auckland University of Technology, Auckland, New Zealand

During the COVID-19 pandemic, wastewater testing for the SARS-CoV-2 virus emerged as a core component of the pandemic response in Aotearoa New Zealand and overseas. This project has addressed key knowledge gaps that emerged during the pandemic regarding how to best deploy wastewater testing in non-traditional settings, how to effectively engage with communities served by such testing, and how to communicate results.

We will describe both a tikanga framework for wastewater surveillance, and the process of developing that framework. This includes consideration of the reasons for testing, sampling methodology, analysis, communication of results, and data sovereignty. We believe this will help drive international conversations about how wastewater-based surveillance progra can be tailored for the benefit of Indigenous communities.

We will also describe developing sampling approaches for the collection of wastewater from aircraft, airports and specific communities such as hospitals. The practicalities of sampling and what analysis of this wastewater can tell us about the bacteria, viruses, protozoa, and fungi that may threaten human health will be illustrated. Appropriate use of quantitative PCR and sequencing technologies for detection of these organis will be explored. We will frame the analytical results in ter of the consideration of the rationale for testing, the significance and certainty of any detection, and how that information might be best used.
Because of this project, Aotearoa New Zealand will be better placed to utilise wastewater-based epidemiology, at a range of scales, for infectious disease response in the future.

From Global Warming to Local Warning: Climate-Health Security and Pandemic Preparedness in Aotearoa/New Zealand

Angela Baschieri[1], Annette Bolton[1], Sarah Jefferies[1], Isabelle Patties, Sherif Ammar, Lucia Rivas, David Murdoch
1 PHF Science, New Zealand

Background: Aotearoa/New Zealand has warmed 1.09°C above pre-industrial levels, intensifying climate-driven hazards such as heat, floods, increase in risks of potential vector incursion, zoonotic spillover, and antimicrobial resistance (AMR)—which compound infectious-disease risks and strain health systems. Global accords (WHO Pandemic Accord 2025; WHO Climate & Health Agreement) call for integrated "health security" strategies.

Methods: We conducted a rapid review of peer-reviewed literature, international case studies, and a semi-systematic environmental scan using a leading large language model and Perplexity.ai's retrieval-augmented system of New Zealand initiatives. We mapped findings against the Health National Adaptation Plan (2024–2027) and the Interim Pandemic Plan (2025).

Results: Four interlinked threats were characterized: heat-driven morbidity exacerbating chronic disease; flood-related waterborne illness via contamination and expanded vector habitats; zoonotic/vector-borne infections shifting transmission dynamics; and A accelerated by higher temperatures, wastewater overflows, agricultural runoff, and extreme-weather dispersal. Five response pillars—early warning systems; One Health coordination; Artificial Intelligence (AI)-driven data integration; resilient health infrastructure; and community-centred adaptation—align with emerging pilots.

Conclusions: A multipronged, layered approach—combining cross-agency data sharing, One Health governance, ethical AI deployment under Te Mana Raraunga, as the Māori Data Sovereignty network, resilient health infrastructure, and community-centred adaptation—will accelerate New Zealand's transition to a pandemic-ready, climate-resilient health system and offer a blueprint for other nations.

Roof harvested drinking water surveillance using metagenomics and qPCR in the Ngāi Tahu Takiwā

Gabe Mulcare[1]
[1] University of Canterbury, Christchurch, New Zealand

Systemic failures in drinking water syste pose significant health risks, with Aotearoa experiencing some of the most severe waterborne disease outbreaks in the developed world. Current microbial water quality testing relies on 19th-century technology, primarily monitoring total colifor and Escherichia coli, which fails to capture the full spectrum of potential pathogens. Metagenomics is redefining how water quality can be managed and offers a powerful DNA sequencing approach that can identify microbes present in a water sample that cannot be cultured in a lab. This study ai to explore metagenomics as a cost-effective surveillance tool for drinking water, addressing critical gaps in current water quality monitoring and supporting indigenous water management capabilities.
The research employs a longitudinal design across 15 roof water sites in a coastal community on private supply, combining metagenomic and quantitative PCR (qPCR) technologies. Water samples have been collected from both source and treated water systems. The first wave of data collected occurred after a period of high bird activity where we expected contamination to be at its worst. A second wave of data collection is planned for a period of low bird activity (September 2025). Nucleic acids are extracted from the samples and prepared for metagenomics sequencing runs using 16S rRNA. qPCR targets the common animal markers to identify contamination sources.

First wave results revealed widespread contamination and diverse bacterial communities, with several opportunistic pathogens detected at varying abundances, and qPCR confirmed the presence of the specific bird d marker. Sites that had a comprehensive treatment system with both filtration and UV had substantially reduced bacterial loads. These findings highlight the potential health risks posed by untreated or inadequately treated roof water and validate the use of more advanced monitoring. This approach offers a comprehensive assessment of bacterial risks and treatment efficacy, supporting informed water safety management.

Linking Treated Water Contamination and Campylobacteriosis Risk Using Explainable Machine Learning

Farnaz Pourzand[1], **Yuming Guo**[2], **Tim Chambers**[3], **Michael Baker**[1], **Simon Hales**[1],
1 Otago University, Wellington, New Zealand, 2 Monash University, Melbourne, Victoria, Australia, 3 Canterbury University, Christchurch, New Zealand

Safe drinking water is critical to preventing enteric infections, yet contamination of treated water supplies still occurs and may contribute to community-level disease burden. In New Zealand, Campylobacter remains the leading cause of notified gastrointestinal illness, with occasional outbreaks linked to drinking water exposure. Understanding how water quality and population characteristics shape disease risk is essential for effective public health response and prevention.
This study applied a spatial machine learning approach to investigate associations between campylobacteriosis notifications and treated water quality indicators, land use, and socio-demographic characteristics at the meshblock level across New Zealand from 2015 to 2019. A Boosted Regression Tree (BRT) model was used to predict disease notifications, incorporating variables such as mean E. coli detection in treated water, water testing frequency, urban–rural classification, population density, age structure, area-level deprivation, and proportion of Māori population. SHapley Additive exPlanations (SHAP) were used to interpret the model and identify the most influential predictors.

The analysis revealed that higher frequencies of water quality testing were d with lower predicted notification rates, potentially reflecting more effective monitoring syste or reduced contamination. In contrast, increased E. coli detection in treated water supplies was positively d with disease risk, particularly when mean detection exceeded 0.2. Interestingly, areas with higher proportions of Māori population were d with lower predicted notification rates, suggesting possible under-ascertainment or differences in healthcare access or reporting.

This study demonstrates the value of explainable machine learning for uncovering spatial and nonlinear relationships in environmental health data. The findings highlight the need for targeted improvements in water quality surveillance and equitable public health strategies, particularly in underserved communities. By integrating environmental and population-level data, this work supports more informed, data-driven interventions to reduce the burden of enteric disease in Aotearoa New Zealand.

Session 9

P1 - Mass burial and carcass disposal practices during Avian Influenza outbreaks: Enhancing New Zealand's Emergency Preparedness

Laura Banasiak[1], **Theo Sarris**[1], **Louise Weaver**[1], **Liping Pang**[1], **Allanah Kenny**[1]
1 New Zealand Institute For Public Health And Forensic Science, Christchurch, Canterbury, New Zealand

Mass poultry mortality during high-pathogenicity avian influenza (HPAI) outbreaks presents serious biosecurity and environmental challenges. Rapid and safe disposal of infected carcasses is essential to prevent the spread of disease and protect water quality. Investigations in New Zealand have confirmed the presence of pathogens such as Clostridium perfringens, enterococci, total coliforms, and Campylobacter in groundwater downgradient of open offal pits. These risks are expected to escalate during emergency culling events, posing threats to human and animal health via contaminated water sources. Historically, New Zealand's burial practices have relied on arbitrary buffer distances and burial depths, without accounting for subsurface variability or burial intensity. This approach lacks a robust scientific basis and may be inadequate during high-volume emergency responses. While international studies offer insights, they often focus on bacterial indicators and overlook viral pathogens, which are critical to protecting receiving waters. This project addresses the environmental and public health risks d with mass on-farm poultry carcass disposal during HPAI outbreaks. In this presentation, we will be presenting a synthesis of global practices from countries with experience in managing such events (e.g., USA, Canada, UK, Netherlands, South Africa, South Korea), our evaluations of pathogen decomposition science, and our assessment of the suitability of New Zealand's landfill infrastructure for emergency disposal. We will be presenting our science-based, culturally appropriate recommendations for the Ministry for Primary Industries (MPI), regional councils, iwi, and the poultry industry. Stakeholder engagement, including MPI, the poultry sector, and Hokonui Rūnanga, has helped identify knowledge gaps and strengthen New Zealand's pandemic preparedness. The project will inform national protocols, support regional planning, and lay the groundwork for future field-based research on virus transport and groundwater contamination. Ultimately, it ai to improve New Zealand's emergency response capacity and safeguard water quality during future infectious disease outbreaks.

P2 - Uncovering virus diversity in urban waterfowl

Lia Heremia[1], **Rebecca French**[1], **Stephanie Waller**[1], **Janelle Wierenga**[1], **Jemma Geoghegan**[2]
1 University Of Otago, Dunedin, Otago, New Zealand, 2 New Zealand Institute for Public Health and Forensic Science, Wellington, New Zealand

Avian species such as waterfowl serve as important viral reservoirs. Their extensive migratory patterns, global distribution and unique adaptive immune syste allow them to play distinctive roles as natural hosts of a vast array of diverse viruses. Throughout history, humans have maintained a close relationship with birds, which has intensified in recent times due to factors such as agriculture and deforestation. These factors, coupled with increased human mobility, heighten the risk of viral spillover events and disease outbreaks. Despite this, we know very little about viruses in Aotearoa's waterfowl, particularly those that inhabit urban ecosystems.
This study uncovered the faecal virome harboured by waterfowl in botanical gardens and city parks across Aotearoa, where interactions between waterfowl and humans are frequent. Using a Metatranscriptomic approach, we assessed the diversity of viruses carried by Aotearoa's urban waterfowl to understand their national-level spread, global connectivity and quantify zoonotic risk.
To this end, we identified viruses across nine viral families including avian influenza virus and coronaviruses. We also found that viromes were remarkably homogeneous across Aotearoa, with no significant clustering in their diversity and abundance. That is, I found no linear association between geographic distance and virome similarity, meaning that it is likely viruses among Aotearoa's urban waterfowl are highly connected by frequent transmission events.

This study has identified viruses that may pose a potential risk for future disease outbreaks, with particular relevance to animal health. This research not only provides valuable insights into the viral diversity among Aotearoa's urban waterfowl but also strengthens infectious disease surveillance efforts.

P3 - Climate variability, seasonal shifts and climate impact on waterborne disease in Aotearoa/New Zealand

Angela Baschieri[1], **Annette Bolton**[1], **Sarah Nelson**[1], **Simon Hales**
1 PHF Science, New Zealand

The Intergovernmental Panel on Climate Change (IPCC) warns that global temperatures are likely to increase by over 2 °C by the end of the 21st century, with some scenarios predicting increases exceeding 3 °C (IPCC, 2023). These changes destabilize ecosyste and intensify extreme weather events, including heavy rainfall, flooding and droughts. Such events significantly im-

pact water and sanitation infrastructure, increasing the risk of waterborne diseases, such as cholera, typhoid, and dysentery (Jung et al., 2023; Levy et al., 2016). Although high-income countries such as New Zealand have relatively resilient infrastructure, events such as the 2016 Campylobacteriosis outbreak in Havelock North triggered by heavy rainfall highlight the vulnerability of robust syste (Gilpin et al., 2020). The pathways linking climate change to waterborne diseases are complex: rising temperatures support pathogen survival, whereas extreme events can overwhelm treatment systems.

We conducted a systematic review of the literature on the impact of climate change and seasonal variability on the incidence of waterborne diseases in New Zealand. Our objectives were to assess current knowledge on mechanistic transmission pathways, identify population vulnerability factors, and evaluate collective evidence to inform adaptation strategies.
We searched PubMed, Web of Science, and Google Scholar for English-language studies published between January 2000 and January 2025. We combined Boolean search strings for climate-related and waterborne disease ter with "New Zealand." Two reviewers independently screened the studies using predefined inclusion and exclusion criteria, and we extract data following the Meta-Analyses Systematic Reviews and Preferred Reporting Ite PRISMA 2020 guidelines. To enhance the review, we also tested three AI-assisted search tools and integrated their results.

The findings highlight climate drivers, especially rising temperatures and extreme rainfall, linked to increased waterborne disease risks, with disproportionate effects on children, rural and Māori populations. We provide evidence-based recommendations to strengthen public health responses and adaptation planning.

P5 - Community-Based Carriage of Neisseria meningitidis and Streptococcus pneumoniae in Pacific Households in South Auckland

Mishal Manisha Naidu[1], **Vaifagaloa Naseri**[3], **Louisa Ryan**[3], **Tai Naseri**[3], **Sue McAllister**[1], **Connor Watene O'Sullivan**[4], **Sarah Jefferies**[2], **Amanda Kvalsvig**[5], **Gerard Sonder**[7], **Emma Best**[6], **Xiaoyun Ren**[2], **Philip Hill**[1]
1 University Of Otago, Dunedin, New Zealand, 2 New Zealand Institute for Public Health and Forensic Science, Wellington, New Zealand, 3 Pasefika Family Health Group, Panmure, Auckland, New Zealand, 4 The Moko Foundation, Kaitaia, New Zealand, 5 University of Otago, Wellington, New Zealand, 6 University of Auckland, Auckland, New Zealand, 7 Pacific Perspectives, Wellington, New Zealand

Background: Invasive meningococcal disease and invasive pneumococcal disease are severe infectious diseases caused by Neisseria meningitidis and Streptococcus pneumoniae, respectively. In Aotearoa, New Zealand, both diseases disproportionately affect Māori and Pacific populations, especially children. We conducted a community-based carriage study in Pacific households in South Auckland to understand carriage and transmission of these bacteria. This is the first community-based carriage study of these pathogens in Aotearoa, New Zealand.

Method: Eligible households were selected from a randomised list from the Pasefika Family Health Group database, and through outreach and community engagement processes. Each household member, or the parent/guardian of children, was interviewed following consent, and their household information, demographic data, medical history, vaccination status, and social and lifestyle data were collected. Nasopharyngeal swabs and oropharyngeal swabs (from those aged 3 years and above) were also taken for the identification of meningococcus and pneumococcus.

Results: From late May to mid-July 2025, recruitment and sample collection were completed for 700 individuals. To date, samples from 381 individuals have been processed, with 141 individuals testing positive for pneumococci and 70 individuals testing positive for meningococci. The percentages positive for pneumococcus and meningococcus are 37% and 18%, respectively. Further data analysis is currently underway.

Conclusion/Significance of Findings: Our study ai to estimate the overall and age-specific prevalence of pneumococcal and meningococcal carriage and to identify potential risk factors d with carriage. These findings will contribute to a better understanding of carriage dynamics in the community and help inform targeted public health strategies.

P6 - Molecular characterisation of Streptococcus pneumoniae and Neisseria meningitidis carriage in the community

Eszter Scarlett-Herbert[1], **Louisa Ryan**[2], **Conor Watene O'Sullivan**[3], **Vai Naseri**[2], **Sue McAllister**[4], **Emma Best**[5], **Sarah Jefferies**[6], **Amanda Kvalsvig**[7], **Gerard Sonder**[8], **James Ussher**[1], **Philip Hill**[4], **Xiaoyun Ren**[6]
1 University Of Otago, Central Dunedin, New Zealand, 2 Pasefika Family Health Group, Panmure, Auckland, New Zealand, 3 The Moko Foundation, Kaitāia, New Zealand, 4 Centre for International Health, Department of Preventive and Social Medicine, University of Otago, Dunedin, New Zealand, 5 Department of Paediatrics Child and Youth Health, School of Medicine, Faculty of Medical and Health Sciences, The University of Auckland, Auckland, New Zealand, 6 New Zealand Institute for Public Health and Forensic Science, Wellington, New Zealand, 7 Department of Public Health, University of Otago, Wellington, New Zealand, 8 Pacific Perspectives Ltd, Wellington, New Zealand

Invasive diseases caused by Streptococcus pneumoniae and Neisseria meningitidis, including meningitis and pneumonia, disproportionately burden Māori and Pasifika communities in New Zealand. However, both pathogens are often part of the normal human microbiome, in a state known as carriage, which is a necessary precursor to disease. This study investigates the carriage of S. pneumoniae and N. meningitidis within Māori households in Kaitāia and Pacific households in South Auckland.

To assess carriage, oropharyngeal and nasopharyngeal swabs were taken from study participants, S. pneumoniae was isolated using Columbia sheep blood agar with gentamicin, while N. meningitidis was isolated on New York City, and on Thayer-Martin agar. To enhance detection sensitivity, we performed DNA extraction followed by real-time PCR, detecting the lytA gene for S. pneumoniae and porA and ctrA genes for N. meningitidis. Subsequently, we applied molecular typing via the Quellung reaction for S. pneumoniae and genomic sequencing for culture-positive S. pneumoniae and N. meningitidis isolates to understand the diversity of circulating strains and provide insights into the transmission of these bacteria within the household. We also aim to identify differences in carriage serotypes compared with New Zealand disease isolates, and to investigate new strain introductions and specific patterns of transmission within households over time, using longitudinal samples.

P8 - Registered Nurses' Views on Te Whata Kura: Aotearoa's Antibiotic Guidelines. Exploring Usability, Relevance, Practice Implications

Gigi Lim, Mark Thomas, Steve Ritchie
1 Faculty of Medical and Health Science University of Auckland, 85 Grafton Road, Auckland, Auckland New Zealand

Statement of the Problem: Registered nurses (RNs) are central to antimicrobial stewardship (AMS), playing key roles in infection prevention, antibiotic administration, patient education, and therapeutic monitoring. However, despite their frontline responsibilities, RNs are rarely consulted in the development of antibiotic guidelines, which are typically tailored for prescribers. This exclusion limits the practical relevance and usability of such guidelines for nursing practice. A newly developed antibiotic guideline in Aotearoa New Zealand (Te Whata Kura) offers a unique opportunity to incorporate nursing perspectives into its refinement and implementation. Understanding how RNs engage with this guideline is essential to ensuring its clinical utility and supporting broader A goals.

Methods: A scoping review of international and national literature was conducted to explore the current state of RN involvement in A and their use of antibiotic guidelines. Insights from the review informed the design of a qualitative study, which will use focus group interviews with RNs from both hospital and community settings to gather feedback on the usability, relevance, and clarity of the new guideline.

Results: The literature review identified a critical gap in guideline development processes that fail to acknowledge nurses as key end-users. Evidence suggests that when nurses are engaged in AMS, prescribing practices and patient outcomes improved [1-3]. However, existing guidelines often do not reflect nursing workflows or decision-making processes [4-6]. Without explicit consideration of the nursing context, guidelines risk limited uptake and reduced effectiveness.

Conclusion: This research is timely and necessary. The inclusion of RN feedback in the development and implementation of the new guideline enhances its relevance, usability, and integration into routine care. By centering the nursing voice, this study ai to promote a more collaborative, interdisciplinary approach to A and ensure that antibiotic guidelines are fit for purpose.

P9 - Patient-reported preferences around intravenous and oral antibiotics for the treatment of Staphylococcus aureus bacteremia

Loughlin McGrath[1,2], Genevieve Walls[1], Michael Trent Herdman[1], Anita J. Campbell[3,4,5], Matthew P. Cheng[6], Michael Marks[7,8,9], Jaap ten Oever[10], Euna Sahng[11], A/ Dafna Yahav[12,13], Steven Y.C. Tong[14,15], Anna L. Goodman[16,17], Anecita Gigi Lim[18], Max Bloomfield[19]
1 Department of Infectious Diseases, Middlemore Hospital, Te Whatu Ora Counties Manukau, Auckland 1640, New Zealand, Auckland, New Zealand, 2 University of Auckland School of Medicine and Health Sciences, New Zealand, Auckland, New Zealand, 3 Department of Infectious Diseases, Perth Children's Hospital, Australia, 4 Wesfarmers Centre of Vaccines and Infectious Diseases, The Kids Research Institute, Australia, 5 School of Medicine, University of Western Australia, Perth, Australia, 6 Division of Infectious Diseases, McGill University, Montreal, Canada, 7 Clinical Research Department, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, UK, 8 Hospital for Tropical Diseases, University College London Hospital, UK, 9 Division of Infection and Immunity, University College London, UK, 10 Department of Internal Medicine and Community for Infectious Diseases, Radbound University Medical Centre, Nijmegen, The Netherlands, 11 Department of Infectious Diseases, Tauranga Hospital, Te Whatu Ora Hauora a Toi Bay of Plenty, New Zealand, 12 Infectious Diseases Unit, Sheba Medical Centre,

Ramat-Gan, Israel, 13 Faculty of Medical and Health Sciences, Tel-Aviv University, Ramat Aviv, Israel, 14 Victorian Infectious Diseases Service, The Royal Melbourne Hospital, at the Peter Doherty Institute for Infection and Immunity, Australia, 15 Department of Infectious Diseases, The University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Australia, 16 Medical Research Council Clinical Trials Unit at University College London, UK, 17 Department of Infection at Guy's and St Thomas' NHS Foundation Trust and King's College London, UK, 18 University of Auckland School of Nursing, Auckland, New Zealand, 19 Department of Infectious Diseases, Wellington Hospital, Te Whatu Ora Capital and Coast, New Zealand

Background: There is growing evidence to support partial oral antibiotic treatment of severe infections such as Staphylococcus aureus bacteremia, but clinical practice is slow to adopt this paradigm. We know little about how patients with severe infection experience and perceive intravenous and oral antibiotics in ter of quality of life and clinical effectiveness. We performed a qualitative study to elicit patients' views on treatment with intravenous and oral antibiotics, aiming to provide insights that could inform collaborative treatment decision-making.

Methods: We conducted semi-structured interviews with participants in the Staphylococcus aureus Network Adaptive Platform trial pharmacological sub-study PR-O-SNAP by telephone, in person, or via video conferencing. Interviews were recorded, transcribed and coded, and used to analyse and identify themes. Interviews occurred in two phases between November 2024 and January 2025, with interim analysis to refine interview questions between each phase.

Results: We interviewed 17 patients who had received sequential intravenous then oral antibiotics for treatment of Staphylococcus aureus bacteremia. Overall, participants preferred oral antibiotics for their convenience, which enabled improved mobility and independence, despite a perception that oral regimens were more complex and likely to cause side effects, and that intravenous antibiotics were more effective.

Conclusions: Choosing a route of antibiotic administration for treatment of severe infection is a nuanced decision which should incorporate not just a patient's clinical status, but also their preferences and personal context. Patient convenience and functional goals should be considered in treatment discussions between clinicians and patients.

P10 - Antimicrobial Susceptibility of Kingella kingae from Australia and New Zealand: Implications for Paediatric Osteoarticular Treatment

Katharina Wolf[1]
1 University of Otago, Christchurch, New Zealand

Kingella kingae is increasingly recognised as a leading cause of osteoarticular infections (OAI) in young children. Although generally susceptible to a broad spectrum of antibiotics, regional susceptibility data remain scarce, particularly in Australasia. In this study, we characterised the antimicrobial iles of 61 K. kingae isolates collected across Australia and New Zealand to inform empirical treatment recommendations, with a focus on first-generation cephalosporins.
Susceptibility testing was performed using broth microdilution, disk diffusion, or both, in accordance with ISO 20776-1:2019 and EUCAST guidelines. All isolates were beta-lactamase negative and showed high susceptibility to penicillin, ampicillin, amoxicillin, and second- and third-generation cephalosporins. Notably, first-generation cephalosporins—particularly cefalexin and cefazolin—demonstrated potent in vitro activity (MICμμ ≤ 2 mg/L). In contrast, flucloxacillin and cloxacillin displayed higher MICμμ values (16 mg/L and 4 mg/L, respectively), indicating limited activity. All isolates were fully susceptible to azithromycin and erythromycin. Interestingly, clavulanic acid markedly lowered amoxicillin MICs, even in the absence of beta-lactamase production, suggesting an intrinsic target interaction.

These findings represent the first regional susceptibility data for K. kingae in Australasia and support the empirical use of first-generation cephalosporins in paediatric OAI. They also underscore the need for EUCAST interpretive criteria specific to K. kingae, particularly for commonly used oral beta-lactams. Further studies across diverse geographic settings are warranted to guide clinical practice and support the development of targeted breakpoints.

P11 – Unprepared and unaware: knowledge gaps in post-infection, post-sepsis recovery

Paul Huggan[1], **Bennett Pomana**
1 Sepsis Trust NZ, Waikato, New Zealand

In lay terms, sepsis is defined as "a life-threatening condition where the body's response to an infection causes damage to its own tissues and organs", or in te reo Maaori as "mate whakataaoke" (toxic illness). It can be caused by bacteria and viruses (including SARS-CoV-2), and its local epidemiology is marked by maldistributed risk, with Maaori and Pacific people facing at least twice the risk of a sepsis episode, independently of known risks such as socioeconomic deprivation, age, and medical co-morbidity.

Sepsis Trust NZ conceives three spaces where sepsis outcomes might be improved, which are community preparedness, health system response, and recovery and rehabilitation; with research underpinning improvements in each.

This talk presents the lived experience of a sepsis episode, as told by Bennett. It highlights the major gaps in research, provider awareness, and community support for survivors of critical illness. Bennett's experience and others illustrate that the long-term effects of critical illness should be an anticipated cost of endemic and pandemic infectious diseases.

P12 - Feasibility of a sustainable community-led response plan for infectious disease

Ngahiraka Dallas[1,2], **Irene Setiawan**[1,2]
1 Te Mātāpuna Hauora, Christchurch, Canterbury, New Zealand, 2 Mahaanui Kurataiao Ltd, Christchurch, Canterbury, New Zealand

Te Pātaka o Rākaihautū Banks Peninsula is a remote rural community, with four Papatipu Rūnanga and residents living in several discrete communities across the peninsula. Te Waihora (Lake Ellesmere), known as Te Kete Ika o Rākaihautū – The Fish Basket of Rākaihautū, is a rural community with one Papatipu Rūnanga. Both regions are characterised by dispersed settlements and geographical isolation, presenting unique challenges in preparing and responding to infectious disease outbreaks.

The aim of this project is to assess the feasibility of developing a sustainable, community-led response plan for infectious disease for Te Pātaka and Te Kete Ika o Rākaihautū, under the guidance of mana whenua and clinical expertise.

The research involves conducting a literature review of lessons learned from Covid-19 responses in rural Māori communities, as well as international best practice models of rural, Indigenous, and community-led responses to infectious disease outbreaks. A wānanga will be held with representatives from each of the five Papatipu Rūnanga to reflect on key findings, incorporate Te Ao Māori perspectives in the context of each marae community, and ground the proposed response in local tikanga and lived rural realities.

Insights from the literature review and wānanga will inform practical recommendations for a mana whenua-led response plan tailored to the needs of these communities. Final recommendations and reflections will be presented alongside discussion of the project's broader relevance for rural Māori public health preparedness of an infectious disease response plan.

P13 - Cultural Safety Training for New Zealand Secondary Prophylaxis Providers for Rheumatic Fever

Anneka Anderson[2], **Monleigh Ikiua**[1], **Manawa Rhind**[1]
1 National Hauora Coalition, Auckland, New Zealand, 2 University of Auckland, Auckland, New Zealand

Acute rheumatic fever (ARF) is an autoimmune response to a Group A Streptococcus (GAS) infection and remains a significant health issue in Aotearoa New Zealand (AoNZ). Māori and Pacific children aged 5 to 14 years experience significantly higher rates of ARF than their non-Māori and non-Pacific counterparts. To prevent further damage, ARF patients receive monthly intramuscular penicillin injections for a minimum of 10 years. However, recent research highlights a gap between ARF services and patients/whānau expectations, including a need for culturally safe care. To address this gap, we delivered cultural safety training to more than 60 Secondary Prophylaxis Providers for rheumatic fever in Waikato. Cultural safety encompasses critical consciousness whereby healthcare essionals are aware of their own values and biases and take responsibility for delivering care that is culturally safe, as defined by the patient and their communities. This presentation will highlight the key elements of the training and the feedback received from participants. Ongoing collaboration with Te Whatu Ora Waikato (New Zealand's primary publicly funded healthcare system) will help refine and expand this training, ensuring healthcare providers are better equipped to engage with Māori and Pacific whānau.

P14 - Pacific youth Risk perceptions on Infectious diseases and Social Media – PRISM study

Jason Tautasi[1], **Luisa Taufa**[1]
1 University of Auckland, Auckland, New Zealand

Introduction: Pacific youth in Aotearoa New Zealand face disproportionate risks from infectious diseases, yet little is known about their perceptions, barriers to care, and preferred health communication strategies. The PRISM study aimed to explore these dimensions to inform culturally responsive interventions.

Methods: A mixed-methods approach was used. Quantitative data were collected via an online survey involving 550 Pacific youth aged 16–35, capturing demographics, risk perception, health literacy, and barriers to care. Qualitative data were ob-

tained from 20 focus group transcripts and were analysed thematically to identify recurring patterns and contextual insights.

Results: Survey results showed moderate concern for rheumatic fever (29%) and respiratory illness (29%), with lower concern for STIs (25%). Health literacy was modest across conditions, with most participants rating their knowledge at 5/10. Key barriers included cost (75%), long wait times (65%), and fear of judgment (49%). Social media was a dominant source of health information, with 90% engagement and 61% reporting behaviour change due to online content. Thematic analysis revealed deep distrust in the health system, stigma around STIs, gendered gaps in mental health support, and a strong preference for culturally safe, youth-friendly services. Participants emphasised the importance of relatable messengers, short-form digital content, and trusted adults in health communication.

Conclusion: Pacific youth are calling for empathetic, culturally grounded healthcare and communication strategies. Addressing systemic barriers and leveraging digital platfor can enhance engagement and improve infectious disease outcomes. These findings offer actionable insights for designing youth-centred public health interventions.

P15 - 16S rRNA sequencing surveillance tool to monitor community drinking water supplies in the Aotea Harbour

Okeroa Waaka[1]
1 University of Waikato – Te Whare Wananga O Waikato, Hamilton, New Zealand

Outbreaks as a result of waterborne illness and diseases are the ultimate consequence of inadequate drinking water systems. Public health will remain at risk from potential outbreaks following contamination events without effective means to monitor and respond. For those who live rurally, there is an even greater risk, as many households will have small, self-supplied domestic water syste that are not covered by drinking water regulations.

Current drinking water standards in Aotearoa, New Zealand (DWSNZ) define the maximum acceptable concentrations of contaminants in safe drinking water. The DWSNZ highlight the detection of indicator organis Escherichia coli and total colifor to assess the bacterial quality of drinking water. This traditional form of water quality testing whilst sufficient, lacks the ability to capture the full microbial ile of organis present in water samples, omitting key insights around sources of contamination. Metagenomic analysis is a rapid and cost-effective technology that can detect, identify, and characterize all microorganis present in water samples, greatly enhancing drinking water surveillance capability.

This study will use such technology in the form of 16S rRNA sequencing, to investigate the seasonal microbial ile of various groundwater sources, rural household tank water systems, and marae tank water syste within the Aotea Harbour. The overall aim of this research project is to ensure the long-term availability of safe drinking water for the rural Māori communities of Aotea Harbour. This research project serves a small step towards upholding the principle of oritetanga in Te Tiriti o Waitangi, by enabling rural whanau Māori the opportunity to have the same level of care, vigilance, and confidence in their drinking water supplies as their urban city counterparts.

This research project is still in the early stages of commencement and therefore final results and conclusions are unavailable at this time.

P16 - Genomic epidemiology of Mycobacterium tuberculosis complex in Fiji

Saki Baleivanualala[1,2], **Timothy Sahai**[3], **James Ussher**[1,4], **Htin Lin Aung**[1]
1 Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand, 2 Fiji National University, Suva, Fiji, 3 Ministry of Health and Medical Services, Suva, Fiji, 4 Awanui Labs, Dunedin Hospital, Dunedin, New Zealand

Tuberculosis (TB) is a major public health concern in Fiji, yet no prior genomic data exist to inform surveillance and control strategies. This study is the first genomic epidemiology investigation in Fiji to characterise the lineage diversity, drug resistance, and transmission dynamics of Mycobacterium tuberculosis complex (MTBC).

A retrospective analysis using convenience sampling was conducted on 66 laboratory-confirmed MTBC isolates collected in 2019-2022 at the Fiji MTB reference laboratory. DNA extraction and whole genome sequencing (WGS) were performed.

Species identification revealed 62 (94%) M. tuberculosis and 4 (6%) M. bovis. M. tuberculosis lineages included lineage 4 (29; 46.8%), lineage 3 (13; 21%), lineage 2 (11; 17.7%), and lineage 1 (9; 14.5%). Lineage 4 was most prevalent, comprising four small clusters primarily linked to household and religious contacts. Sub-lineage 4.3.3 was predominant (21; 72%). Comparison with New Zealand's 4.3.3 strain showed no close genetic relationship, suggesting independent evolution or separate introduction sources for lineage 4 in Fiji. The lineage 3 cluster comprised eight genetically linked isolates, of which four had confirmed epidemiological links in a transmission chain spanning a school, household contacts, social gatherings, and church participation;

the remaining four lacked epidemiological data.

Overall, five of the 62 MTB isolates were drug-resistant, including one isoniazid mono-resistant in lineage 4, two polyresistant and one mono-resistant case in lineage 2, and one polyresistant case in lineage 1. No multidrug-resistant TB was detected. This first genomic study of MTBC in Fiji demonstrates the value of WGS for iling drug-resistance, detecting both localised outbreaks and broader transmission patterns, guiding targeted interventions, and strengthening national TB control efforts.

P17 - CRISPR-Cas12a detection of Mycobacterium leprae DNA in human samples for the diagnosis of leprosy

Amy Scott-Thomas[1], Elizabeth Chernysheva[1], Patrick Campbell[1,2], Allison Miller[1], Stephen Chambers[1], Trevor Anderson[3], Nicholas Douglas[2,4,5], Martin Kennedy[1]
1 Department of Pathology and Biomedical Science, University of Otago, Christchurch, New Zealand, 2 Department of Infectious Diseases, Christchurch Hospital, Te Whatu Ora Waitaha, New Zealand, 3 Canterbury Health Laboratories, Christchurch, New Zealand, 4 Department of Medicine, University of Otago, Christchurch, New Zealand, 5 Division of Global and Tropical Health, Menzies School of Health Research, Charles Darwin University, Darwin, Australia

Introduction: Leprosy, also known as Hansen's Disease (HD), is a chronic bacterial infection caused by Mycobacterium leprae. Leprosy is a neglected tropical disease which is still endemic to many parts of the world including Africa, Asia, South America, and parts of the Pacific; a worldwide average of 200,000 cases of leprosy is reported every year. If left untreated this disease can cause permanent disabilities such as blindness and nerve damage. Treatment in the early stages of disease can prevent disability, but the lack of testing in endemic regions, as well as the increasing rates of antibiotic-resistant infections pose a significant threat to public health. In addition to the physical deformities and disabilities caused by HD, the religious and social stigma d with this disease continues to ostracize the people affected.

Materials and methods: Latest advancements in the field of microbial diagnostics employ CRISPR-Cas enzyme complexes for the detection of pathogen DNA in various human samples. Our group has designed and optimised a CRISPR-Cas12a based assay for the detection of M. leprae DNA in human skin biopsies and nasal swabs. Clinical validation was performed on skin biopsy and nasal swab samples in a cohort of N=343 leprosy patients from the island country of Kiribati.

Results: In vitro modelling experiments and clinical validation demonstrate that the CRISPR assay has excellent specificity and is more sensitive than the current gold-standard diagnostic method of RT-qPCR detection of M. leprae DNA.

Conclusions: The development and deployment of a point-of-care molecular diagnostic tool for leprosy would bolster testing, leading to improved patient outcomes, a better understanding of the disease epidemiology, and slowing the rate of antimicrobial resistance development due to more targeted antibiotic use.

P18 - Development of a urine-based bacterial cell-free DNA test for Legionnaires' disease

Amy Scott-Thomas[1], Masuma Zawari[1], Trevor Anderson[2], Elizabeth Chernysheva[1], Stephen T. Chambers[1], Michael Maze[3], Malina Storer[4]
1 Department of Pathology and Biomedical Sciences, University Of Otago, Christchurch, Christchurch, New Zealand, 2 Canterbury Health Laboratories, Christchurch, New Zealand, 3 Department of Medicine, University of Otago, Christchurch, Christchurch, New Zealand, 4 Canterbury Respiratory Research Group, Canterbury District Health Board, Christchurch, New Zealand

Introduction: Legionnaires' disease (LD) is a severe form of community-acquired pneumonia that cannot be radiographically distinguished from pneumonias caused by other pathogens. While Legionella pneumophila is the most commonly recognised cause worldwide, Legionella longbeachae is the predominant cause of LD in New Zealand. Despite its clinical significance, LD remains underdiagnosed, partly due to difficulties in obtaining sputum samples for PCR or culture. This study aimed to evaluate the potential of a cell-free DNA hybridisation assay for the detection of Legionella DNA in urine samples as a more sensitive diagnostic tool.

Materials and methods: Urine samples were spiked with known concentrations of fragmented Legionella DNA to evaluate the performance of the hybridisation assay, which utilised Legionella-specific probes. DNA extraction efficiency and detection sensitivity of the hybridisation assay were compared against a commercial extraction kit and the phenolchloroform extraction method.

Results: The hybridisation assay demonstrated a sensitivity of 90% and a specificity of 100%. It outperformed both the commercial kit and the phenol-chloroform method in consistently detecting Legionella longbeachae and Legionella pneumophila DNA in urine samples.

Conclusions: The DNA hybridisation assay showed high sensitivity and specificity for the detection of fragmented Legionella DNA in urine and offers a promising alternative for diagnosing LD, particularly in patients unable to provide sputum samples. Incorporating this assay into routine diagnostics in New Zealand could significantly improve LD detection rates.

P19 - Detection of Legionella cell-free DNA in blood for the non-invasive diagnosis of Legionnaires' Disease

Amy Scott-Thomas[1], Elizabeth Chernysheva[1], Masuma Zawari[1], Allison Miller[1], Stephen Chambers[1], Michael Maze[2,3], Malina Storer[4], Martin Kennedy[1]
1 Department of Pathology and Biomedical Science, University of Otago, Christchurch, New Zealand, 2 Department of Respiratory Medicine, Canterbury District Health Board, Christchurch, New Zealand, 3 Department of Medicine, University of Otago, Christchurch, New Zealand, 4 Canterbury Respiratory Research Group, Canterbury District Health Board, Christchurch, New Zealand

Introduction: Legionnaires' disease (LD) is a severe form of community-acquired pneumonia and is a well-documented occurrence worldwide. However, due to inconsistent testing, this illness often goes undiagnosed leading to empiric treatment and excess use of broad-spectrum antibiotics. LD cannot be clinically or radiographically distinguished from other types of pneumonia, so current diagnostics are reliant on sputum samples and testing for the presence of Legionella bacteria using culture-based or PCR-based techniques. However, these methods have limited applicability in population groups who cannot provide sputum, such as older or intubated patients.

Materials and methods: Latest advancements in the field of microbial diagnostics employ clustered, short palindromic repeats (CRISPR) and CRISPR d protein (Cas) enzyme complexes for the detection of pathogen nucleic acids in human blood samples. Previous work from our group has shown that Legionella cell-free DNA is present in the blood and urine of patients with Legionnaires' Disease.
We propose that Legionella cell-free DNA circulating in the human bloodstream can be used as a non-invasive biomarker for the diagnosis of Legionnaires' disease.

Results: Our group has designed and optimised a CRISPR-Cas12a-based assay for the detection of Legionella DNA in human blood. We have carried out several in vitro modelling experiments to demonstrate the robust specificity and sensitivity of this assay, as well as ensuring that this system can detect the highly fragmented pathogen cfDNA found in plasma. We will soon begin clinical validation of this assay using blood samples from the ADEPT cohort of patients admitted with pneumonia to Christchurch Hospital, Canterbury, New Zealand.

Conclusions: The availability of a non-invasive test for Legionnaires' disease would bolster testing, leading to improved patient outcomes, a better understanding of the disease epidemiology, and slowing the rate of antimicrobial resistance development due to more targeted antibiotic use.

P20 - Mechanis of immune escape by hypervirulent strains of Mycobacterium tuberculosis

Naomi Daniels[1], Taru Dutt[2], Philip Hill[1,3], Marcela Henao-Tamayo[2], Jo Kirman[1]
1 University Of Otago, Dunedin, New Zealand, 2 Colorado State University, Fort Collins, Colorado, USA, 3 Centre for International Health, University of Otago, Dunedin, New Zealand

Tuberculosis (TB), a lung disease caused by Mycobacterium tuberculosis (Mtb), remains the world's leading cause of death from infectious disease. In New Zealand, approximately 300 new cases are notified each year. The bacille Calmette–Guérin (BCG) vaccine prevents disease in ~50% of cases, but how BCG protects—or fails to protect—remains incompletely understood. Notably, BCG provides little to no protection against TB caused by Beijing-genotype Mtb strains; linked to large-scale outbreaks, global spread, and multidrug-resistant TB. Our research ai to understand why BCG is ineffective against this high-risk lineage and to identify immune pathways that may be targeted in future vaccine strategies.

We used a mouse aerosol infection model with clinical Mtb isolates: a Beijing strain and a globally common Lineage 4 (L4) strain. Lung tissues were analysed using spatial transcriptomics, allowing us to map gene activity and immune responses across the lung microenvironment. We also isolated BCG-trained alveolar macrophages to directly assess how effectively they controlled growth of Beijing or L4 Mtb.

Infection with the Beijing strain led to markedly altered immune responses in the lung compared to infection with L4. Key immune defence pathways - including those involved in inflammation, antigen presentation, and immune cell metabolism - were suppressed. Genes involved in recognising and responding to infection were downregulated, while genes linked with immune evasion were upregulated. These effects were reflected functionally: BCG-trained alveolar macrophages were less able to

control growth of Beijing Mtb than L4.

These findings suggest that Beijing Mtb disrupts host immunity at multiple levels, even in BCG-vaccinated hosts. This may help explain BCG's reduced efficacy against hypervirulent strains and highlights immune pathways that could be targeted in future vaccine design. Our results also shed light on which aspects of BCG-induced immunity are most essential - and most vulnerable - to immune evasion.

P21 - Investigating the role of the TNFAIP3 T108A/I207L genetic variant in immune response to infectious disease

Emma Duffy[1,5], Zsolt Komlosi[2], Thaize Chometon[3], Colleen Higgins[1], Natalie Netzler[4,5], Chris Puli'uvea[1,5]
1 School of Science, Auckland University of Technology, New Zealand, 2 Department of Genetics, Cell and Immunobiology, Semmelweis University, Hungary, 3 Faculty of Science, University of Auckland, New Zealand, 4 Faculty of Medical and Health Sciences, University of Auckland, New Zealand, 5 Maurice Wilkins Centre, New Zealand

Tumour Necrosis Factor Induced Protein 3 (TNFAIP3) encodes the A20 protein, a key negative regulator of the NF-μB signalling pathway, with deubiquitinating (DUB) enzyme activity. Inefficient inhibition of this pathway by A20 has been shown to drive many inflammatory disorders, highlighting its key role in regulating immune homeostasis. Understanding the role of genetic variations in TNFAIP3 on immune function may improve our understanding of variations in immune responses to infection. A unique TNFAIP3 variant T108A/I207L is enriched in Māori and Pacific populations but is virtually absent in other populations. The T108A/I207L variants are found in cis, located close to the active site of the DUB enzyme activity, indicating a potentially influential role in protein stability, activity and function. Furthermore, the orthologous T108A/I207L variant confers viral resistance in mice. This study ai to determine the role of the TNFAIP3 T108A/I207L variant in human immune responses to infectious diseases. Here, we present our workflow for participant recruitment and immunophenotyping. Here we show preliminary results revealing variations in immune cell composition when comparing those with and without the TNFAIP3 T108A/I207L variant. Results from this study will provide us with a better understanding of this genetic variant and its role in immune function and variation. This may help lay the foundations for precision medicine for these population groups.

P22 - Safety of aH5N6c Influenza Vaccinations in Adults Primed with aH5N1c or Unprimed (V89_18E1)

Eve Versage[1], Esther Van Twuijver[2], Robert L. Jacobs[3], Matthew Hohenboken[1]
1 CSL Seqirus, Waltham, Massachusetts, USA, 2 CSL Seqirus, Amsterdam, Netherlands, 3 Biogenics Research Institute, San Antonio, Texas, USA

Background: A prior Phase 3 study (V89_18) evaluated the immunogenicity and safety of an MF59-adjuvanted, cell-based H5N1 pandemic vaccine (aH5N1c) in healthy adults. Subjects were asked to participate in an extension study (V89_18E1) to evaluate the safety of two aH5N1c priming doses followed by booster vaccinations with aH5N6c 3 weeks apart. Immunogenicity results have been reported separately.

Methods: 258 subjects were evaluated. Primed subjects, who had received 2 aH5N1c doses were randomized 1:1 to receive aH5N6c Day 1 and aH5N6c or saline placebo on Day 22. H5 naïve subjects received two aH5N6c vaccinations, 3 weeks apart. Adverse event (AE) observation extended from first vaccination until study completion. AEs were collected as either unsolicited or solicited AEs (reactogenicity) collected for 7 consecutive days following vaccination.

Results: Reactogenicity within 7 days after any vaccination was similar across treatment groups. Injection site pain was the most frequently reported solicited local AE. The most frequently reported solicited systemic AEs were fatigue, headache and malaise. Most solicited AEs were mild/moderate in intensity, with onset close to vaccination, and resolved within 3 days. Rates of solicited AEs were lower after the second vaccination than the first vaccination. Receipt of a third or fourth dose of MF59-adjuvanted H5 vaccine in primed subjects did not result in increased reactogenicity. From Day 1 through Day 43, the proportion of subjects reporting at least 1 unsolicited AE was similar across treatment groups. The majority of unsolicited AEs were mild. The overall incidence of SAEs was low and none were considered related to the study vaccine.

Conclusions: Vaccinations with aH5N6c were well tolerated and no safety concerns were identified. Repeated dosing with an MF59-adjuvanted H5 vaccine did not result in increased reactogenicity. The safety ile observed in this trial was consistent with that of other MF59-adjuvanted monovalent cell-based influenza vaccines.

P23 - Immunogenicity of aH5N6c Influenza Vaccinations in Adults Primed with aH5N1c or Unprimed (V89_18E1)

Esther Van Twuijver[1], Eve Versage[2], Robert L. Jacobs[3], Matthew Hohenboken[2]
1 CSL Seqirus, Amsterdam, Netherlands, 2 CSL Seqirus, Waltham, Massachusetts, USA, 3 Biogenics Research Institute, San Antonio, Texas, USA

Background: A prior Phase 3 study (V89_18) evaluated immunogenicity and safety of cell-based H5N1 pandemic vaccine (aH5N1c) in healthy adults. Subjects were asked to participate in an extension study (V89_18E1) to evaluate whether two aH5N1c priming doses followed by booster vaccinations with aH5N6c 3 weeks apart elicit immune responses to priming (H5N1) antigens.

Methods: 260 subjects were enrolled. Primed subjects, who had received 2 aH5N1c doses were randomized 1:1 to receive aH5N6c on Day 1 and aH5N6c or saline placebo on Day 22. H5 naïve subjects received two aH5N6c vaccinations, 3 weeks apart. Blood samples were collected on Days 1, 8, 22, 43. Immunogenicity was assessed by HI and MN assays against the heterologous H5N1 strain in the priming vaccine.

Results: Following a single aH5N6c vaccination, a rapid immune response against the H5N1 strain in primed subjects was observed as early as Day 8 and further increased at 3 weeks after the first vaccination. No further increase was observed 3 weeks after the second vaccination for primed subjects who received 1 or 2 aH5N6c vaccinations. In H5 naïve subjects, immune responses against the H5N1 strain were minimal. Primed subjects met both CBER criteria against the H5N1 strain at 3 weeks after the first and second vaccination. H5 naïve subjects did not meet any CBER criterion against the H5N1 strain.

Conclusions: In aH5N1c primed subjects, 1 or 2 aH5N6c booster vaccinations elicited similar robust immune responses against the H5N1 strain. In H5 naïve subjects, 2 vaccinations with aH5N6c elicited lower immune responses against the H5N1 strain compared to primed subjects. The results indicate that cross-reactive antibodies can be elicited after a primary series of aH5N1c following one or two MF59-adjuvanted booster vaccinations with a genetically diverse H5 strain, suggesting immune memory persists for at least 6 years after initial vaccinations.

P24 - Developing a Multisite Database for Background Rates of Adverse Events for Vaccine Evaluation in Africa

Luam Ghebreab[1], Jennifer Griffin[1], Yannan Jiang[1], Kimberley Gutu[2], Jessica Ann Yun[2], Husna Ismail[2], Hazel Clothier[1], William Dormechele [3], Arier Lee[1], Clare L. Cutland[2], Jim Buttery[1], Steven B. Black[1]
[1] Global Vaccine Data Network, Auckland, New Zealand, [2] Wits African Leadership in Vaccinology Expertise (Wits-Alive), School of Pathology, Faculty of Health Science, University of the Witwatersrand, Johannesburg, South Africa, [3] Navrongo Health Research Centre, Navrongo, Ghana

Background rates of adverse events following immunisation (AEFI) are critical for effective vaccine safety surveillance, enabling rapid detection and assessment of potential vaccine safety signals. However, such data are often lacking in low- and middle-income countries (LMICs), limiting the ability to conduct robust vaccine safety monitoring. The BRAVE (Background Rates for Adverse Events of Vaccination Evaluation) project ai to establish a harmonised, centralised database to collect and analyse baseline rates of AEFI across multiple sites in four African countries to strengthen vaccine safety monitoring in LMICs.

A secure REDCap (Research Electronic Data Capture) database was developed as the central repository linking all project sites to support harmonised data collection and management. REDCap was selected for its flexibility, scalability, and ability to support standardised, comparable data collection across diverse settings. The study protocol was translated into standardised electronic case report forms, site-specific data flows were designed, and both logical and physical database structures were implemented.
Development challenges included complex calculations and logic, variable internet connectivity, and diverse regulatory requirements. These were addressed through statistical software validation of complex rules, deployment of the REDCap mobile offline app, and tailoring workflows to site contexts while maintaining both local and international compliance standards. The BRAVE database enables centralised, real-time, quality-assured data collection and monitoring across all sites, ensuring standardised and comparable data for AEFI background rate estimation.

The BRAVE REDCap database demonstrates the feasibility and benefits of a harmonised, centralised data platform for managing complex, multisite vaccine safety studies in resource-limited African settings and offers a scalable model for strengthening global vaccine safety surveillance.

P25 - HPV vaccination in Aotearoa New Zealand: Coverage achieved under school-based and primary-care-based programmes.

Sarah Cosgrove[1], Phil Hider[1], Tony Walls[2], Research Andy Anglemeyer[3]
1 Department of Population Health, University of Otago, Christchurch, New Zealand, 2 Department of Paediatrics and Child Health, University of Otago, Christchurch, New Zealand, 3 Department of Preventative and Social Medicine, University of Otago, Dunedin, New Zealand

Immunisation against the Human Papillomavirus (HPV) was introduced into Aotearoa New Zealand's (NZ) national schedule in 2008, with three doses of the vaccine primarily being delivered through a school-based vaccination programme (SBVP) to girls in year 8. Canterbury was the only exception, and instead delivered HPV vaccines through primary healthcare providers (PCPs) from 2008 to 2015, and then through a combination of schools and PCPs from 2016 onwards. From 2017 onwards boys aged 12 to 13 were included in the programme. The aim of this study was to investigate the impact of these differing approaches to HPV vaccination of coverage amongst adolescents.

To investigate these trends, one-dose coverage from 2013 to 2023 was analysed amongst adolescents born 13 years earlier using vaccination data from the Aotearoa Immunisation Register.

Amongst female adolescents' coverage was lower in Canterbury than non-Canterbury from 2013 to 2018. Canterbury coverage increased significantly from 2016, when the mixed model programme was introduced, to 2019. Male coverage from 2017 to 2023 was consistent. Canterbury female's coverage from 2013 to 2020 was consistent across the European, Māori and Pacific populations, whereas in non-Canterbury coverage was consistently lower amongst European females. Māori and Pacific males in Canterbury had lower coverage than European males until 2020, whereas Māori and European males in non-Canterbury had equal coverage. In 2020, under the COVID-19 pandemic, coverage decreased more in Canterbury than non-Canterbury, and decreased more amongst Māori and Pacific adolescents than European.

School-based approaches to HPV vaccine delivery amongst adolescents in NZ tended to be more effective than a PCP-based or mixed model approach, and appeared to be more successful at achieving high coverage amongst Māori and Pacific communities. This research can inform developments to NZ's HPV vaccination programmes to ensure coverage is high and consistent across different locations, ethnicities, and genders.

Session 10

Are we still on target? – insights from ARROW New Zealand

Cameron Grant[1], Marisa van Arragon[2], Tania Milne[1], Alicia Stanley[2], Vasemaca Moi[2], April Ly[2], Jane Fata[2], Reena Ho[2], Simone Watkins[1], Arun Gangakhedkar[4], Owen Sinclair[4], Lorraine Torrance[4], Louise Guy[4], Rebecca Alekzander[5], Shirley Lawrence[5], Gail Spence[5], Laarni Tundag[5], Maricar Santiago[5], Rakyang Lee[5], Alex Wallace[6], Julia Laing[6], Rachael Healey[6], Cilla Wyllie-Schmidt[6], Kristen Mead[6], Angus Goodson[7], Anita Lala[7], Jolene Reid[7], Julia Reid[7], Brooke Shergold[7], Laurel Teoh[8], Rose Ann Yap[8], Natasha Eagle[8], Thomas Saunders[9], Rachel Teulon[9], Jessica Costa-Pinto[10], Peter Vuillermin[10], Sarah McNab[11], Peter Sly[12]
1 Department of Paediatrics: Child & Youth Health, University Of Auckland, Auckland, New Zealand, 2 Te Whatu Ora – Health New Zealand Te Toka Tumai, Auckland, New Zealand, 3 Te Whatu Ora – Health New Zealand Te Tai Tokerau, Whangārai, New Zealand, 4 Te Whatu Ora – Health New Zealand Waitematā, Auckland, New Zealand, 5 Te Whatu Ora – Health New Zealand Counties Manukau, Auckland, New Zealand, 6 Te Whatu Ora – Health New Zealand Waikato, Hamilton, New Zealand, 7 Te Whatu Ora – Health New Zealand Hauora a Toi Bay of Plenty, Tauranga, New Zealand, 8 Te Whatu Ora – Health New Zealand Capital, Coast and Hutt Valley, Wellington, New Zealand, 9 Te Whatu Ora – Health New Zealand Waitaha Canterbury, Christchurch, New Zealand, 10 Deakin University, Geelong, Australia, 11 Royal Melbourne Children's Hospital, Melbourne, Australia, 12 University of Queensland, Queensland, Australia

The ARROW study Assessing the Reduction of Recurrent admissions using OM85 for preschool Wheeze (ARROW) is a RCT that will determine if preschool wheeze readmissions can be prevented with an oral vaccine.

Although the ARROW study began in January 2019, recruitment commenced in 2023 following an extended preparatory phase. Now, after 17 grant applications and with recruitment concluding in December 2025, what have we learned?

We are reminded every day that the time, energy and creativity used to make our study video was so worthwhile. We are reminded every day that kanohi ki te kanohi visits are worth the early starts, long travelling distances and late finishes.

We have formed stronger relationships with people we have worked alongside for a long time. Some never expected to become involved in research. Some now find themselves on their own postgraduate education journey.

We have formed new relationships with people we would otherwise not have met. ARROW provided a kōrero start point for us to work together to improve child health. We look forward to the journey these relationships will continue to take us on.

As of August 2025, we have enrolled 225 tamariki in Aotearoa. By prioritizing high-burden cases, we achieved greater statistical power per participant, allowing for a reduction in the required sample size.

ARROW reminded us of the importance of the patient's voice and the reality of the frustration and stress for whānau living with preschool wheeze and the imperfections of our healthcare system. The study attrition rate is low. Hence the required sample size reduced further.

Beyond scientific outcomes, ARROW has created opportunities for essional and personal growth, relationship development, for excellent science, reciprocity and resilience. Many unexpected challenges provided countless opportunities to help one another find good ways forward.

Pacific youth Risk perceptions on Infectious diseases and Social Media – PRISM study

Jason Tautasi[1], **Luisa Taufa**[1]
1 University of Auckland, Auckland, New Zealand

Introduction: Pacific youth in Aotearoa New Zealand face disproportionate risks from infectious diseases, yet little is known about their perceptions, barriers to care, and preferred health communication strategies. The PRISM study aimed to explore these dimensions to inform culturally responsive interventions.

Methods: A mixed-methods approach was used. Quantitative data were collected via an online survey involving 550 Pacific youth aged 16–35, capturing demographics, risk perception, health literacy, and barriers to care. Qualitative data were obtained from 20 focus group transcripts and were analysed thematically to identify recurring patterns and contextual insights.

Results: Survey results showed moderate concern for rheumatic fever (29%) and respiratory illness (29%), with lower concern for STIs (25%). Health literacy was modest across conditions, with most participants rating their knowledge at 5/10. Key barriers included cost (75%), long wait times (65%), and fear of judgment (49%). Social media was a dominant source of health information, with 90% engagement and 61% reporting behaviour change due to online content. Thematic analysis revealed deep distrust in the health system, stigma around STIs, gendered gaps in mental health support, and a strong preference for culturally safe, youth-friendly services. Participants emphasised the importance of relatable messengers, short-form digital content, and trusted adults in health communication.

Conclusion: Pacific youth are calling for empathetic, culturally grounded healthcare and communication strategies. Addressing systemic barriers and leveraging digital platfor can enhance engagement and improve infectious disease outcomes. These findings offer actionable insights for designing youth-centred public health interventions.

Empowering Aboriginal (Australia) and Torres Strait Islander Voices Through Involvement and Consultation

Bryony Roberts[1]
1 First Nations Pandemic Research Preparedness Network (first), Melbourne, VIC, Australia

First Nations Peoples of Australia are recognised as a priority population, but despite targeted pandemic responses, continue to experience ongoing health inequities. First Nations Peoples' experiences, values and perspectives need to be embedded into disease control strategies and responses. First Nations Community Panels have been found to effectively engage communities in decision-making about infectious disease emergencies and offers a way for government health authorities to work collaboratively with First Nations Peoples, in two-way learning, understanding and communication in the design of public health policy.
To date, we have conducted seven First Nations Community Panels across four Australian states to assess First Nations Peoples' informed views through a deliberative process on topics such as pandemic influenza, and COVID-19 strategies. Panels were asked to make decisions on priority levels, coverage, and vaccine doses.

Using the First Nations Community Panels methodology, we aim to build understanding of the preferences, values, and opinions of First Nations communities when creating policy and public health strategies. Additionally, we aim to ensure that First Nations voices are central in decision-making processes related to public health, policy and research.

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Māori whānau experiences of critical illness in Wellington Intensive Care Unit

Jackson Smeed-Tauroa[1]
1 Medical Research Institute Of New Zealand, Wellington, Wellington, New Zealand

Intensive Care Units [ICU] are critical spaces in healthcare, where whānau of patients can face significant emotional challenges. This may be heightened during pandemics where there have been restrictions on travel and visiting. In Aotearoa, little is known about the experiences of patients' whānau, and whether current practice aligns with Te Ao Māori, making this a critical area to improve pandemic preparedness. The first step to provide best practice recommendations for future pandemics, is to describe how current practices impact our whānau. Māori are a collectivist culture, and being present to care for and support their whānau is important for both the patient and their whānau. This study ai to understand how the well-being of whānau of Māori patients can be supported while their whānau is being cared for in an ICU.

Guided by Kaupapa Māori, this research is exploring the kōrero shared by whānau of Māori patients about their experiences in an ICU and how this effects their hauora. While analysis is incomplete, preliminary findings indicate huge whānau support, descending from across the motu to support their loved ones. Whānau have to deal with the stress of their whānau being critically unwell, while also being in an environment surrounded by others who are critically unwell. Lessons learned from this study will help to address the challenges posed by future pandemics, add literature to aid in pandemic preparedness that is culturally responsive to the needs of Māori and their whānau.

Map


Overflow carpark
Carpark
Rourou Iti
Assembly area for Pōwhiri
Kimiora - Conference dinner
Pare Waikato
Main confernce entrance
Kimikimi (ground floor), Pare Hauraki (upstairs)
Main confernce location

Acknowledgements

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The Tuurangawaewae team under Glenda Raumati's leadership made it possible for us to return to this important site - Ngaa mihi nui for hosting us. Thank you to the Tainui Waikato Endowed College team. Thank you to Professor Marama Lanning for supporting the organisation.

Te Kawenata o Te Niwha

Te Niwha Charter

Te Whakakitenga | Vision

Aotearoa New Zealand's response to current, ongoing and emerging infectious disease threats is characterised domestically and internationally as a strong, prepared and unified network.

Te Ahunga | Mission

To ensure Aotearoa New Zealand has world-class research capability to support our preparedness for current and future infectious disease challenges.

Te Tuatahi | Article One

Kāwanatanga | Governorship

Obligation to protect Māori rights

- Representation & kaitiakitanga
- Structural mechanisms
- Decision-making partnership

Te Tuarua | Article Two

Tino Rangatiratanga | Self-Determination

Māori exercising authority over their affairs

- Engaged, involved
- Capacity & capability building
- Design & implementation

Te Tuatoru | Article Three

Ōritetanga | Equity

Protection and rights

- Equitable outcomes
- Tikanga & kawa
- Mana enhancement & due regard

A tātou Mātāpono | Our Principles

	Tiakitanga | Accountability	Hononga | Relationships	Tūhonotanga | Partnerships	Rangatiratanga | Leadership
	We are accountable to those involved in or affected by the conduct of our research.	**Our connection to each other, through shared work and experience, provides a sense of belonging.**	**We commit to healthy relationships that are transparent, positively impactful and honourable.**	**We bring people together, encouraging participation, and developing future leaders.**

Ngā Tikanga | Our Values

Kia pono ai **Integrity**	Actively strive for research excellence, demonstrate the highest standards of behaviour and foster a culture of integrity.	Understand the impact of your role and relationship within the research ecosystem.	Partner with tāngata tiriti, tāngata whenua, where we undertake rangahau for whom there are reasonably foreseeable direct impacts.	Act with honesty and transparency. Disclose and manage conflicts of interest. Acknowledge those who have contributed and acknowledge relevant work by others.
Aroha **Respect & compassion**	Understand and implement all ethical, tikanga, kawa, and regulatory requirements and standards.	Reach into Mana Whenua and communities when undertaking rangahau to recognise their mana and respect their interests, aspirations and priorities.	Exhibit respect for individuals and communities. Nurture cultural confidence through an appreciation of diversity of thought and values.	Reflect on the consequences of research for communities. Disseminate results and findings and feedback findings to communities.
Mahi tahi **Collaboration**	Behave with openness, honesty, professionalism, responsibility and integrity to safeguard the health, safety, wellbeing and rights of communities.	Actively seek collaboration with partners across different disciplines, organisations, and diverse communities.	Engage in bi-directional learning to advance and enhance the benefit of collaborations	Ensure partnerships contribute to building capacity by supporting the development of future research leaders.
Kotahitanga **Unity**	Use appropriate methodologies that are collaboratively designed and collaboratively delivered with research partners.	Acknowledge the expertise and disciplines of research partners and communities.	Seek to understand, learn and appreciate the aspirations of all partners.	Lead and influence to ensure the health and wellbeing of our communities are supported by everyone.